Sequence Listing

<110> Avi J. Ashkenazi
Kevin P. Baker
David A. Botstein
Luc Desnoyers
Dan L. Eaton
Napoleone Ferrara
Sherman Fong
Wei-Qiang Gao
Hanspeter Gerber
Mary E. Gerritsen
Audrey Goddard
Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
James Pan
Nicholas F. Paoni
Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
Colin K. Watanabe
P.Mickey Williams
William I. Wood
Zemin Zang

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caggctgccc  cgctgacggc  cagggtgaag  catgtgagga  gccgccccgg  450

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His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn Gln Ser Glu
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Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
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His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn
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Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly
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Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe
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Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln
            350             355             360

Gly Asn Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg
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Lys Val Phe Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser
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                35                  40                  45

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Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser
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Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp
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Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys
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Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu
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Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn
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Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser
               155                 160                 165

Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met
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Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu
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14

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 tctacactct  tcaacctcat  accagtggga  ctacgtgttg  ttgccatcca  350

 gggagtgaaa  acagggttgt  atatagccat  gaatggagaa  ggttacctct  400

 acccatcaga  acttttttacc  cctgaatgca  agtttaaaga  atctgttttt  450

 gaaaattatt  atgtaatcta  ctcatccatg  ttgtacagac  aacaggaatc  500

 tggtagagcc  tggtttttgg  gattaaataa  ggaagggcaa  gctatgaaag  550

 ggaacagagt  aaagaaaacc  aaaccagcag  ctcattttct  acccaagcca  600

 ttggaagttg  ccatgtaccg  agaaccatct  ttgcatgatg  ttggggaaac  650

 ggtcccgaag  cctgggggtga  cgccaagtaa  aagcacaagt  gcgtctgcaa  700

 taatgaatgg  aggcaaacca  gtcaacaaga  gtaagacaac  atag  744
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<210> 13
<211> 247
<212> PRT
<213> Homo Sapien

<400> 13

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 Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln
   1               5                  10                      15

 Ala Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg
                    20                    25                    30
```

```
Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val
                35                  40                      45

Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg
                50                  55                      60

Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu
                65                  70                      75

Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala
                80                  85                      90

Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn
                95                  100                     105

Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys
                110                 115                     120

Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro
                125                 130                     135

Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe
                140                 145                     150

Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln
                155                 160                     165

Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln
                170                 175                     180

Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His
                185                 190                     195

Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser
                200                 205                     210

Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro
                215                 220                     225

Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro
                230                 235                     240

Val Asn Lys Ser Lys Thr Thr
                245
```

<210> 14
<211> 2609
<212> DNA
<213> Homo Sapien

<400> 14
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 ctcgcagccg agcgcggccg gggaagggct ctccttccag cgccgagcac 50

 tgggccctgg cagacgcccc aagattgttg tgaggagtct agccagttgg 100

 tgagcgctgt aatctgaacc agctgtgtcc agactgaggc cccatttgca 150

 ttgtttaaca tacttagaaa atgaagtgtt cattttaac attcctcctc 200
```

16

caattggttt aatgctgaat tactgaagag ggctaagcaa aaccaggtgc 250

ttgcgctgag ggctctgcag tggctgggag gacccggcg ctctccccgt 300

gtcctctcca cgactcgctc ggcccctctg gaataaaaca cccgcgagcc 350

ccgagggccc agaggaggcc gacgtgcccg agctcctccg ggggtcccgc 400

ccgcgagctt tcttctcgcc ttcgcatctc ctcctcgcgc gtcttggaca 450

tgccaggaat aaaaaggata ctcactgtta ccattctggc tctctgtctt 500

ccaagccctg ggaatgcaca ggcacagtgc acgaatggct ttgacctgga 550

tcgccagtca ggacagtgtt tagatattga tgaatgccga accatccccg 600

aggcctgccg aggagacatg atgtgtgtta accaaaatgg cgggtattta 650

tgcattcccc ggacaaaccc tgtgtatcga gggccctact cgaacccta 700

ctcgaccccc tactcaggtc cgtacccagc agctgcccca ccactctcag 750

ctccaaacta tcccacgatc tccaggcctc ttatatgccg ctttggatac 800

cagatggatg aaagcaacca atgtgtggat gtggacgagt gtgcaacaga 850

ttcccaccag tgcaacccca cccagatctg catcaatact gaaggcgggt 900

acacctgctc ctgcaccgac ggatattggc ttctggaagg ccagtgctta 950

gacattgatg aatgtcgcta tggttactgc cagcagctct gtgcgaatgt 1000

tcctggatcc tattcttgta catgcaaccc tggtttacc ctcaatgagg 1050

atggaaggtc ttgccaagat gtgaacgagt gtgccaccga gaaccccctgc 1100

gtgcaaacct gcgtcaacac ctacggctct ctcatctgcc gctgtgaccc 1150

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gcagcttctc tgagttcctc tgccaacatg agtgtgtgaa ccagcccggc 1250

acatacttct gctcctgccc tccaggctac atcctgctgg atgacaaccg 1300

aagctgccaa gacatcaacg aatgtgagca caggaaccac acgtgcaacc 1350

tgcagcagac gtgctacaat ttacaagggg gcttcaaatg catcgacccc 1400

atccgctgtg aggagcctta tctgaggatc agtgataacc gctgtatgtg 1450

tcctgctgag aaccctggct gcagagacca gccctttacc atcttgtacc 1500

gggacatgga cgtggtgtca ggacgctccg ttcccgctga catcttccaa 1550

atgcaagcca cgacccgcta ccctggggcc tattacattt tccagatcaa 1600

atctgggaat gagggcagag aattttacat gcggcaaacg ggccccatca 1650

gtgccaccct ggtgatgaca cgccccatca aagggccccg ggaaatccag 1700

ctggacttgg aaatgatcac tgtcaacact gtcatcaact tcagaggcag 1750

ctccgtgatc cgactgcgga tatatgtgtc gcagtaccca ttctgagcct 1800

cgggctggag cctccgacgc tgcctctcat tggcaccaag ggacaggaga 1850

agagaggaaa taacagagag aatgagagcg acacagacgt taggcatttc 1900

ctgctgaacg tttccccgaa gagtcagccc cgacttcctg actctcacct 1950

gtactattgc agacctgtca ccctgcagga cttgccaccc ccagttccta 2000

tgacacagtt atcaaaaagt attatcattg ctcccctgat agaagattgt 2050

tggtgaattt tcaaggcctt cagtttattt ccactatttt caaagaaaat 2100

agattaggtt tgcgggggtc tgagtctatg ttcaaagact gtgaacagct 2150

tgctgtcact tcttcacctc ttccactcct tctctcactg tgttactgct 2200

ttgcaaagac ccgggagctg gcggggaacc ctgggagtag ctagtttgct 2250

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ggttttttaga gaatgtgttt caaaaccatg cctggtattt tcaaccataa 2350

aagaagtttc agttgtcctt aaatttgtat aacggtttaa ttctgtcttg 2400

ttcattttga gtatttttaa aaaatatgtc gtagaattcc ttcgaaaggc 2450

cttcagacac atgctatgtt ctgtcttccc aaacccagtc tcctctccat 2500

tttagcccag tgttttcttt gaggacccct taatcttgct ttctttagaa 2550

tttttaccca attggattgg aatgcagagg tctccaaact gattaaatat 2600

ttgaagaga 2609

<210> 15
<211> 448
<212> PRT
<213> Homo Sapien

<400> 15

```
Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu
 1               5               10                  15

Cys Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly
                20               25                  30

Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu
                35               40                  45

Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
                50               55                  60
```

```
Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val
                65                    70                    75

Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly
                80                    85                    90

Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro
                95                   100                   105

Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp
               110                   115                   120

Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser
               125                   130                   135

His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly
               140                   145                   150

Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln
               155                   160                   165

Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu
               170                   175                   180

Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
               185                   190                   195

Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu
               200                   205                   210

Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr
               215                   220                   225

Gly Ser Leu Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
               230                   235                   240

Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
               245                   250                   255

Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe
               260                   265                   270

Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser
               275                   280                   285

Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn
               290                   295                   300

Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile
               305                   310                   315

Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn
               320                   325                   330

Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro
               335                   340                   345

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser
```

19

```
                350                     355                     360
      Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro
                    365                     370                     375

      Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg
                    380                     385                     390

      Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val
                    395                     400                     405

      Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu
                    410                     415                     420

      Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser
                    425                     430                     435

      Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
                    440                     445
```

<210> 16
<211> 2447
<212> DNA
<213> Homo Sapien

<400> 16
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 caggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatcctc 50

 tagagatccc tcgacctcga cccacgcgtc cgaacacagg tccttgttgc 100

 tgcagagaag cagttgtttt gctggaagga gggagtgcgc gggctgcccc 150

 gggctcctcc ctgccgcctc ctctcagtgg atggttccag gcaccctgtc 200

 tggggcaggg agggcacagg cctgcacatc gaaggtgggg tgggaccagg 250

 ctgcccctcg ccccagcatc caagtcctcc cttgggcgcc cgtggccctg 300

 cagactctca gggctaaggt cctctgttgc tttttggttc caccttagaa 350

 gaggctccgc ttgactaaga gtagcttgaa ggaggcacca tgcaggagct 400

 gcatctgctc tggtgggcgc ttctcctggg cctggctcag gcctgccctg 450

 agccctgcga ctgtggggaa aagtatggct tccagatcgc cgactgtgcc 500

 taccgcgacc tagaatccgt gccgcctggc ttcccggcca atgtgactac 550

 actgagcctg tcagccaacc ggctgccagg cttgccggag ggtgccttca 600

 gggaggtgcc cctgctgcag tcgctgtggc tggcacacaa tgagatccgc 650

 acggtggccg ccggagccct ggcctctctg agccatctca gagcctgga 700

 cctcagccac aatctcatct ctgactttgc ctggagcgac ctgcacaacc 750

 tcagtgccct ccaattgctc aagatggaca gcaacgagct gaccttcatc 800
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20

cccgcgacg ccttccgcag cctccgtgct ctgcgctcgc tgcaactcaa 850

ccacaaccgc ttgcacacat tggccgaggg caccttcacc ccgctcaccg 900

cgctgtccca cctgcagatc aacgagaacc ccttcgactg cacctgcggc 950

atcgtgtggc tcaagacatg ggccctgacc acggccgtgt ccatcccgga 1000

gcaggacaac atcgcctgca cctcacccca tgtgctcaag ggtacaccgc 1050

tgagccgcct gccgccactg ccatgctcgg cgccctcagt gcagctcagc 1100

taccaaccca gccaggatgg tgccgagctg cggcctggtt ttgtgctggc 1150

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tccagatacc cagtggcatt gtggagatca ccagccccaa cgtgggcact 1250

gatgggcgtg ccctgcctgg cacccctgtg gccagctccc agccgcgctt 1300

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aggaaggcac ctacagctgc ctggccacca tgagctgggg cagtgctgag 1400

agctcagtgg acgtggcact ggccacgccc ggtgagggtg gtgaggacac 1450

actggggcgc aggttccatg gcaaagcggt tgagggaaag ggctgctata 1500

cggttgacaa cgaggtgcag ccatcagggc cggaggacaa tgtggtcatc 1550

atctacctca gccgtgctgg gaaccctgag gctgcagtcg cagaaggggt 1600

ccctgggcag ctgcccccag gcctgctcct gctgggccaa agcctcctcc 1650

tcttcttctt cctcacctcc ttctagcccc acccagggct tccctaactc 1700

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tggcaactcc tgaggcctgc atgggtgact tcacattttc ctacctctcc 1800

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tccaggcact gtgactgtca agctggcaag ggccaggatt gggggaatgg 2050

agctggggct tagctgggag gtggtctgaa gcagacaggg aatgggagag 2100

gaggatggga agtagacagt ggctggtatg gctctgaggc tccctggggc 2150

ctgctcaagc tcctcctgct ccttgctgtt ttctgatgat ttggggggctt 2200

gggagtccct ttgtcctcat ctgagactga aatgtgggga tccaggatgg 2250

ccttccttcc tcttacccctt cctccctcag cctgcaacct ctatcctgga 2300

acctgtcctc cctttctccc caactatgca tctgttgtct gctcctctgc 2350

aaaggccagc cagcttggga gcagcagaga aataaacagc atttctgatg 2400

ccaaaaaaaa aaaaaaaaa gggcggccgc gactctagag tcgacct 2447

<210> 17
<211> 428
<212> PRT
<213> Homo Sapien

<400> 17

```
Met Gln Glu Leu His Leu Leu Trp Trp Ala Leu Leu Leu Gly Leu
 1               5                  10                  15

Ala Gln Ala Cys Pro Glu Pro Cys Asp Cys Gly Glu Lys Tyr Gly
                20                  25                  30

Phe Gln Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro
                35                  40                  45

Pro Gly Phe Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn
                50                  55                  60

Arg Leu Pro Gly Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu
                65                  70                  75

Leu Gln Ser Leu Trp Leu Ala His Asn Glu Ile Arg Thr Val Ala
                80                  85                  90

Ala Gly Ala Leu Ala Ser Leu Ser His Leu Lys Ser Leu Asp Leu
                95                  100                 105

Ser His Asn Leu Ile Ser Asp Phe Ala Trp Ser Asp Leu His Asn
                110                 115                 120

Leu Ser Ala Leu Gln Leu Leu Lys Met Asp Ser Asn Glu Leu Thr
                125                 130                 135

Phe Ile Pro Arg Asp Ala Phe Arg Ser Leu Arg Ala Leu Arg Ser
                140                 145                 150

Leu Gln Leu Asn His Asn Arg Leu His Thr Leu Ala Glu Gly Thr
                155                 160                 165

Phe Thr Pro Leu Thr Ala Leu Ser His Leu Gln Ile Asn Glu Asn
                170                 175                 180

Pro Phe Asp Cys Thr Cys Gly Ile Val Trp Leu Lys Thr Trp Ala
                185                 190                 195

Leu Thr Thr Ala Val Ser Ile Pro Glu Gln Asp Asn Ile Ala Cys
                200                 205                 210

Thr Ser Pro His Val Leu Lys Gly Thr Pro Leu Ser Arg Leu Pro
                215                 220                 225
```

22

```
      Pro Leu Pro Cys Ser Ala Pro Ser Val Gln Leu Ser Tyr Gln Pro
                      230             235                 240

      Ser Gln Asp Gly Ala Glu Leu Arg Pro Gly Phe Val Leu Ala Leu
                      245             250                 255

      His Cys Asp Val Asp Gly Gln Pro Ala Pro Gln Leu His Trp His
                      260             265                 270

      Ile Gln Ile Pro Ser Gly Ile Val Glu Ile Thr Ser Pro Asn Val
                      275             280                 285

      Gly Thr Asp Gly Arg Ala Leu Pro Gly Thr Pro Val Ala Ser Ser
                      290             295                 300

      Gln Pro Arg Phe Gln Ala Phe Ala Asn Gly Ser Leu Leu Ile Pro
                      305             310                 315

      Asp Phe Gly Lys Leu Glu Glu Gly Thr Tyr Ser Cys Leu Ala Thr
                      320             325                 330

      Asn Glu Leu Gly Ser Ala Glu Ser Ser Val Asp Val Ala Leu Ala
                      335             340                 345

      Thr Pro Gly Glu Gly Gly Glu Asp Thr Leu Gly Arg Arg Phe His
                      350             355                 360

      Gly Lys Ala Val Glu Gly Lys Gly Cys Tyr Thr Val Asp Asn Glu
                      365             370                 375

      Val Gln Pro Ser Gly Pro Glu Asp Asn Val Val Ile Ile Tyr Leu
                      380             385                 390

      Ser Arg Ala Gly Asn Pro Glu Ala Ala Val Ala Glu Gly Val Pro
                      395             400                 405

      Gly Gln Leu Pro Pro Gly Leu Leu Leu Leu Gly Gln Ser Leu Leu
                      410             415                 420

      Leu Phe Phe Phe Leu Thr Ser Phe
                      425
```

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
 gtggctggca cacaatgaga tc 22

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

23

<220>
<223> Synthetic oligonucleotide probe

<400> 19
 ccaatgtgtg caagcggttg tg 22

<210> 20
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
 tcaagagcct ggacctcagc cacaatctca tctctgactt tgcctggagc 50

<210> 21
<211> 2033
<212> DNA
<213> Homo Sapien

<400> 21
 ccaggccggg aggcgacgcg cccagccgtc taaacgggaa cagccctggc 50

 tgagggagct gcagcgcagc agagtatctg acggcgccag gttgcgtagg 100

 tgcggcacga ggagttttcc cggcagcgag gaggtcctga gcagcatggc 150

 ccggaggagc gccttccctg ccgccgcgct ctggctctgg agcatcctcc 200

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 ctgtacctat ggatcgatgc tcaccaggca agagtactca taggatttga 300

 agaagatatc ctgattgttt cagaggggaa aatggcacct tttacacatg 350

 atttcagaaa agcgcaacag agaatgccag ctattcctgt caatatccat 400

 tccatgaatt ttacctggca agctgcaggg caggcagaat acttctatga 450

 attcctgtcc ttgcgctccc tggataaagg catcatggca gatccaaccg 500

 tcaatgtccc tctgctggga acagtgcctc acaaggcatc agttgttcaa 550

 gttggtttcc catgtcttgg aaaacaggat ggggtggcag catttgaagt 600

 ggatgtgatt gttatgaatt ctgaaggcaa caccattctc caaacacctc 650

 aaaatgctat cttctttaaa acatgtcaac aagctgagtg cccaggcggg 700

 tgccgaaatg gaggcttttg taatgaaaga cgcatctgcg agtgtcctga 750

 tgggttccac ggacctcact gtgagaaagc cctttgtacc ccacgatgta 800

 tgaatggtgg actttgtgtg actcctggtt tctgcatctg cccacctgga 850

 ttctatggag tgaactgtga caaagcaaac tgctcaacca cctgctttaa 900

24

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tggagggacc tgtttctacc ctggaaaatg tatttgccct ccaggactag 950

agggagagca gtgtgaaatc agcaaatgcc cacaaccctg tcgaaatgga 1000

ggtaaatgca ttggtaaaag caaatgtaag tgttccaaag gttaccaggg 1050

agacctctgt tcaaagcctg tctgcgagcc tggctgtggt gcacatggaa 1100

cctgccatga acccaacaaa tgccaatgtc aagaaggttg gcatggaaga 1150

cactgcaata aaaggtacga agccagcctc atacatgccc tgaggccagc 1200

aggcgcccag ctcaggcagc acacgccttc acttaaaaag gccgaggagc 1250

ggcgggatcc acctgaatcc aattacatct ggtgaactcc gacatctgaa 1300

acgttttaag ttacaccaag ttcatagcct ttgttaacct ttcatgtgtt 1350

gaatgttcaa ataatgttca ttacacttaa gaatactggc ctgaatttta 1400

ttagcttcat tataaatcac tgagctgata tttactcttc cttttaagtt 1450

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ttgggacaga ttttatatta tgtcaattga tcaggttaaa attttcagtg 1550

tgtagttggc agatattttc aaaattacaa tgcatttatg gtgtctgggg 1600

gcagggaac atcagaaagg ttaaattggg caaaaatgcg taagtcacaa 1650

gaatttggat ggtgcagtta atgttgaagt tacagcattt cagattttat 1700

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taaactctca atacaatata ttttgacctt accattattc cagagattca 1800

gtattaaaaa aaaaaaaatt acactgtggt agtggcattt aaacaatata 1850

atatattcta aacacaatga aatagggaat ataatgtatg aacttttgc 1900

attggcttga agcaatataa tatattgtaa acaaaacaca gctcttacct 1950

aataaacatt ttatactgtt tgtatgtata aaataaaggt gctgctttag 2000

ttttttggaa aaaaaaaaa aaaaaaaaa aaa 2033
```

<210> 22
<211> 379
<212> PRT
<213> Homo Sapien

<400> 22

```
Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp
1               5                   10                  15

Ser Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro
                    20                  25                  30
```

```
Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala
                 35              40              45

Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu
                 50              55              60

Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln
                 65              70              75

Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr
                 80              85              90

Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser
                 95              100             105

Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn
                 110             115             120

Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln
                 125             130             135

Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe
                 140             145             150

Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu
                 155             160             165

Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala
                 170             175             180

Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg
                 185             190             195

Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu
                 200             205             210

Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys Val
                 215             220             225

Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
                 230             235             240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr
                 245             250             255

Cys Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly
                 260             265             270

Glu Gln Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly
                 275             280             285

Gly Lys Cys Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr
                 290             295             300

Gln Gly Asp Leu Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly
                 305             310             315

Ala His Gly Thr Cys His Glu Pro Asn Lys Cys Gln Cys Gln Glu
```

26

```
                    320                      325                       330

     Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Glu Ala Ser Leu
                    335                      340                       345

     Ile His Ala Leu Arg Pro Ala Gly Ala Gln Leu Arg Gln His Thr
                    350                      355                       360

     Pro Ser Leu Lys Lys Ala Glu Glu Arg Arg Asp Pro Pro Glu Ser
                    365                      370                       375

     Asn Tyr Ile Trp
```

<210> 23
<211> 783
<212> DNA
<213> Homo Sapien

<400> 23

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 agaacctcag aaatgtgagt tatttgggaa tggctgtttg taaatgtcct 50

 tacgtaagcc aagaggaggt cttgacttgg ggtcccaggg gtaccgcaga 100

 tcccagggac tggagcagca ctagcaagct ctggaggatg agccaggagt 150

 ctggaattga ggctgagcca agacccccag ggccgtctca gtctcataaa 200

 aggggatcag gcaggaggag tttgggagaa acctgagaag ggcctgattt 250

 gcagcatcat gatgggcctc tccttggcct ctgctgtgct cctggcctcc 300

 ctcctgagtc tccaccttgg aactgccaca cgtgggagtg acatatccaa 350

 gacctgctgc ttccaataca gccacaagcc ccttccctgg acctgggtgc 400

 gaagctatga attcaccagt aacagctgct cccagcgggc tgtgatattc 450

 actaccaaaa gaggcaagaa agtctgtacc catccaagga aaaaatgggt 500

 gcaaaaatac atttctttac tgaaaactcc gaaacaattg tgactcagct 550

 gaattttcat ccgaggacgc ttggaccccg ctcttggctc tgcagccctc 600

 tggggagcct gcggaatctt ttctgaaggc tacatggacc cgctggggag 650

 gagagggtgt ttcctcccag agttacttta ataaaggttg ttcatagagt 700

 tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 750

 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 783
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<210> 24
<211> 94
<212> PRT
<213> Homo Sapien

<400> 24

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Met Met Gly Leu Ser Leu Ala Ser Ala Val Leu Leu Ala Ser Leu
 1               5                  10                  15

Leu Ser Leu His Leu Gly Thr Ala Thr Arg Gly Ser Asp Ile Ser
                20                  25                  30

Lys Thr Cys Cys Phe Gln Tyr Ser His Lys Pro Leu Pro Trp Thr
                35                  40                  45

Trp Val Arg Ser Tyr Glu Phe Thr Ser Asn Ser Cys Ser Gln Arg
                50                  55                  60

Ala Val Ile Phe Thr Thr Lys Arg Gly Lys Lys Val Cys Thr His
                65                  70                  75

Pro Arg Lys Lys Trp Val Gln Lys Tyr Ile Ser Leu Leu Lys Thr
                80                  85                  90

Pro Lys Gln Leu
```

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<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
 ggatcaggca ggaggagttt ggg 23

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
 ggatgggtac agactttctt gcc 23

<210> 27
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
 atgatgggcc tctccttggc ctctgctgtg ctcctggcct ccctcctgag 50

<210> 28
<211> 3552
<212> DNA
<213> Homo Sapien
```

<400> 28
gcgagaacct ttgcacgcgc acaaactacg gggacgattt ctgattgatt 50

tttggcgctt tcgatccacc ctcctccctt ctcatgggac tttggggaca 100

aagcgtcccg accgcctcga gcgctcgagc agggcgctat ccaggagcca 150

ggacagcgtc gggaaccaga ccatggctcc tggaccccaa gatccttaag 200

ttcgtcgtct tcatcgtcgc ggttctgctg ccggtccggg ttgactctgc 250

caccatcccc cggcaggacg aagttcccca gcagacagtg gccccacagc 300

aacagaggcg cagcctcaag gaggaggagt gtccagcagg atctcataga 350

tcagaatata ctggagcctg taacccgtgc acagagggtg tggattacac 400

cattgcttcc aacaatttgc cttcttgcct gctatgtaca gtttgtaaat 450

caggtcaaac aaataaaagt tcctgtacca cgaccagaga caccgtgtgt 500

cagtgtgaaa aaggaagctt ccaggataaa aactcccctg agatgtgccg 550

gacgtgtaga acagggtgtc ccagagggat ggtcaaggtc agtaattgta 600

cgccccggag tgacatcaag tgcaaaaatg aatcagctgc cagttccact 650

gggaaaccc cagcagcgga ggagacagtg accaccatcc tggggatgct 700

tgcctctccc tatcactacc ttatcatcat agtggtttta gtcatcattt 750

tagctgtggt tgtggttggc ttttcatgtc ggaagaaatt catttcttac 800

ctcaaaggca tctgctcagg tggtggagga ggtcccgaac gtgtgcacag 850

agtcctttc cggcggcgtt catgtccttc acgagttcct ggggcggagg 900

acaatgcccg caacgagacc ctgagtaaca gatacttgca gcccacccag 950

gtctctgagc aggaaatcca aggtcaggag ctggcagagc taacaggtgt 1000

gactgtagag tcgccagagg agccacagcg tctgctggaa caggcagaag 1050

ctgaagggtg tcagaggagg aggctgctgg ttccagtgaa tgacgctgac 1100

tccgctgaca tcagcacctt gctggatgcc tcggcaacac tggaagaagg 1150

acatgcaaag gaaacaattc aggaccaact ggtgggctcc gaaaagctct 1200

tttatgaaga agatgaggca ggctctgcta cgtcctgcct gtgaaagaat 1250

ctcttcagga aaccagagct tccctcattt accttttctc ctacaaaggg 1300

aagcagcctg gaagaaacag tccagtactt gacccatgcc ccaacaaact 1350

ctactatcca atatggggca gcttaccaat ggtcctagaa ctttgttaac 1400

gcacttggag taattttat gaaatactgc gtgtgataag caaacgggag 1450

29

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aaatttatat cagattcttg gctgcatagt tatacgattg tgtattaagg 1500

gtcgttttag gccacatgcg gtggctcatg cctgtaatcc cagcactttg 1550

ataggctgag gcaggtggat tgcttgagct cgggagtttg agaccagcct 1600

catcaacaca gtgaaactcc atctcaattt aaaaagaaaa aaagtggttt 1650

taggatgtca ttctttgcag ttcttcatca tgagacaagt ctttttttct 1700

gcttcttata ttgcaagctc catctctact ggtgtgtgca tttaatgaca 1750

tctaactaca gatgccgcac agccacaatg ctttgcctta tagttttta 1800

actttagaac gggattatct tgttattacc tgtattttca gtttcggata 1850

tttttgactt aatgatgaga ttatcaagac gtagccctat gctaagtcat 1900

gagcatatgg acttacgagg gttcgactta gagttttgag ctttaagata 1950

ggattattgg ggcttacccc caccttaatt agagaaacat ttatattgct 2000

tactactgta ggctgtacat ctcttttccg atttttgtat aatgatgtaa 2050

acatggaaaa actttaggaa atgcacttat taggctgttt acatgggttg 2100

cctggataca aatcagcagt caaaaatgac taaaaatata actagtgacg 2150

gagggagaaa tcctccctct gtgggaggca cttactgcat tccagttctc 2200

cctcctgcgc cctgagactg gaccagggtt tgatggctgg cagcttctca 2250

aggggcagct tgtcttactt gttaatttta gaggtatata gccatattta 2300

tttataaata aatatttatt tatttattta taagtagatg tttacatatg 2350

cccaggattt tgaagagcct ggtatctttg ggaagccatg tgtctggttt 2400

gtcgtgctgg gacagtcatg ggactgcatc ttccgacttg tccacagcag 2450

atgaggacag tgagaattaa gttagatccg agactgcgaa gagcttctct 2500

ttcaagcgcc attacagttg aacgttagtg aatcttgagc ctcatttggg 2550

ctcagggcag agcaggtgtt tatctgcccc ggcatctgcc atggcatcaa 2600

gagggaagag tggacggtgc ttgggaatgg tgtgaaatgg ttgccgactc 2650

aggcatggat gggcccctct cgcttctggt ggtctgtgaa ctgagtccct 2700

gggatgcctt ttagggcaga gattcctgag ctgcgtttta gggtacagat 2750

tccctgtttg aggagcttgg cccctctgta agcatctgac tcatctcaga 2800

gatatcaatt cttaaacact gtgacaacgg gatctaaaat ggctgacaca 2850

tttgtccttg tgtcacgttc cattatttta tttaaaaacc tcagtaatcg 2900
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30

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ttttagcttc tttccagcaa actcttctcc acagtagccc agtcgtggta 2950

ggataaatta cggatatagt cattctaggg gtttcagtct tttccatctc 3000

aaggcattgt gtgttttgtt ccgggactgg tttggctggg acaaagttag 3050

aactgcctga agttcgcaca ttcagattgt tgtgtccatg gagttttagg 3100

aggggatggc ctttccggtc ttcgcacttc catcctctcc cacttccatc 3150

tggcgtccca caccttgtcc cctgcacttc tggatgacac agggtgctgc 3200

tgcctcctag tctttgcctt tgctgggcct tctgtgcagg agacttggtc 3250

tcaaagctca gagagagcca gtccggtccc agctcctttg tcccttcctc 3300

agaggccttc cttgaagatg catctagact accagcctta tcagtgttta 3350

agcttattcc tttaacataa gcttcctgac aacatgaaat tgttgggggtt 3400

ttttggcgtt ggttgatttg tttaggtttt gctttatacc cgggccaaat 3450

agcacataac acctggttat atatgaaata ctcatatgtt tatgaccaaa 3500

ataaatatga aacctcatrt taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3550

aa 3552
```

<210> 29
<211> 386
<212> PRT
<213> Homo Sapien

<400> 29

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Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
 1               5                  10                  15

Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
             20                  25                  30

Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
             35                  40                  45

Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
             50                  55                  60

Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
             65                  70                  75

Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
             80                  85                  90

Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
             95                  100                 105

Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
             110                 115                 120
```

31

```
Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
            125                 130                 135

Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
            140                 145                 150

Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
            155                 160                 165

Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
            170                 175                 180

Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
            185                 190                 195

Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
            200                 205                 210

His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val
            215                 220                 225

Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
            230                 235                 240

Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His
            245                 250                 255

Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
            260                 265                 270

Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
            275                 280                 285

Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
            290                 295                 300

Ala Glu Leu Thr Gly Val Thr Val Glu Ser Pro Glu Glu Pro Gln
            305                 310                 315

Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
            320                 325                 330

Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
            335                 340                 345

Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
            350                 355                 360

Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
            365                 370                 375

Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
            380                 385
```

<210> 30
<211> 50
<212> DNA
<213> Artificial Sequence

<400> 30
 cataaaagtt cctgcaccat gaccagagac acagtgtgtc agtgtaaaga 50

<210> 31
<211> 963
<212> DNA
<213> Homo Sapien

<400> 31
 gcggcacctg gaagatgcgc ccattggctg gtggcctgct caaggtggtg 50

 ttcgtggtct tcgcctcctt gtgtgcctgg tattcggggt acctgctcgc 100

 agagctcatt ccagatgcac ccctgtccag tgctgcctat agcatccgca 150

 gcatcgggga gaggcctgtc ctcaaagctc cagtccccaa aaggcaaaaa 200

 tgtgaccact ggactccctg cccatctgac acctatgcct acaggttact 250

 cagcggaggt ggcagaagca agtacgccaa aatctgcttt gaggataacc 300

 tacttatggg agaacagctg ggaaatgttg ccagaggaat aaacattgcc 350

 attgtcaact atgtaactgg gaatgtgaca gcaacacgat gttttgatat 400

 gtatgaaggc gataactctg gaccgatgac aaagtttatt cagagtgctg 450

 ctccaaaatc cctgctcttc atggtgacct atgacgacgg aagcacaaga 500

 ctgaataacg atgccaagaa tgccatagaa gcacttggaa gtaaagaaat 550

 caggaacatg aaattcaggt ctagctgggt atttattgca gcaaaaggct 600

 tggaactccc ttccgaaatt cagagagaaa agatcaacca ctctgatgct 650

 aagaacaaca gatattctgg ctggcctgca gagatccaga tagaaggctg 700

 catacccaaa gaacgaagct gacactgcag ggtcctgagt aaatgtgttc 750

 tgtataaaca aatgcagctg gaatcgctca agaatcttat ttttctaaat 800

 ccaacagccc atatttgatg agtattttgg gtttgttgta aaccaatgaa 850

 catttgctag ttgtatcaaa tcttggtacg cagtattttt ataccagtat 900

 tttatgtagt gaagatgtca attagcagga aactaaaatg aatggaaatt 950

 cttaaaaaaa aaa 963

<210> 32
<211> 235
<212> PRT
<213> Homo Sapien

<400> 32

```
Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
 1               5                  10                  15

Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
               20                  25                  30

Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
               35                  40                  45

Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
               50                  55                  60

Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
               65                  70                  75

Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
               80                  85                  90

Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
               95                  100                 105

Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
               110                 115                 120

Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
               125                 130                 135

Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
               140                 145                 150

Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
               155                 160                 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
               170                 175                 180

Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
               185                 190                 195

Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
               200                 205                 210

Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
               215                 220                 225

Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
               230                 235
```

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ggctggcctg cagagatc 18

34

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
 aatgtgacca ctggactccc 20

<210> 35
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 35
 aggcttggaa ctcccttc 18

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
 aagattcttg agcgattcca gctg 24

<210> 37
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
 aatccctgct cttcatggtg acctatgacg acggaagcac aagactg 47

<210> 38
<211> 1215
<212> DNA
<213> Homo Sapien

<400> 38
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 cccgtccctc ccgccgaagc tccgtcccgc ccgcgggccg gctccgccct 100

 cacctcccgg ccgcggctgc cctctgcccg ggttgtccaa gatggagggc 150

 gctccaccgg ggtcgctcgc cctccggctc ctgctgttcg tggcgctacc 200

cgcctccggc tggctgacga cgggcgcccc cgagccgccg ccgctgtccg 250

gagccccaca ggacggcatc agaattaatg taactacact gaaagatgat 300

ggggacatat ctaaacagca ggttgttctt aacataacct atgagagtgg 350

acaggtgtat gtaaatgact tacctgtaaa tagtggtgta acccgaataa 400

gctgtcagac tttgatagtg aagaatgaaa atcttgaaaa tttggaggaa 450

aaagaatatt ttggaattgt cagtgtaagg attttagttc atgagtggcc 500

tatgacatct ggttccagtt tgcaactaat tgtcattcaa gaagaggtag 550

tagagattga tggaaaacaa gttcagcaaa aggatgtcac tgaaattgat 600

attttagtta agaaccgggg agtactcaga cattcaaact ataccctccc 650

tttggaagaa agcatgctct actctatttc tcgagacagt gacattttat 700

ttacccttcc taacctctcc aaaaaagaaa gtgttagttc actgcaaacc 750

actagccagt atcttatcag gaatgtggaa accactgtag atgaagatgt 800

tttacctggc aagttacctg aaactcctct cagagcagag ccgccatctt 850

catataaggt aatgtgtcag tggatggaaa agtttagaaa agatctgtgt 900

aggttctgga gcaacgtttt cccagtattc tttcagtttt tgaacatcat 950

ggtggttgga attacaggag cagctgtggt aataaccatc ttaaaggtgt 1000

ttttcccagt ttctgaatac aaaggaattc ttcagttgga taaagtggac 1050

gtcatacctg tgacagctat caacttatat ccagatggtc cagagaaaag 1100

agctgaaaac cttgaagata aaacatgtat ttaaaacgcc atctcatatc 1150

atggactccg aagtagcctg ttgcctccaa atttgccact tgaatataat 1200

tttctttaaa tcgtt 1215

<210> 39
<211> 330
<212> PRT
<213> Homo Sapien

<400> 39
Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Leu
1   5   10   15

Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro
            20   25   30

Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile
            35   40   45

Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln

36

```
                  50                      55                      60
Val Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn
                65                      70                      75

Asp Leu Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr
                80                      85                      90

Leu Ile Val Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu
                95                     100                     105

Tyr Phe Gly Ile Val Ser Val Arg Ile Leu Val His Glu Trp Pro
               110                     115                     120

Met Thr Ser Gly Ser Ser Leu Gln Leu Ile Val Ile Gln Glu Glu
               125                     130                     135

Val Val Glu Ile Asp Gly Lys Gln Val Gln Gln Lys Asp Val Thr
               140                     145                     150

Glu Ile Asp Ile Leu Val Lys Asn Arg Gly Val Leu Arg His Ser
               155                     160                     165

Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu Tyr Ser Ile Ser
               170                     175     .                 180

Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu Ser Lys Lys
               185                     190                     195`

Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu Ile Arg
               200                     205                     210

Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys Leu
               215                     220                     225

Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val
               230                     235                     240

Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe
               245                     250                     255

Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met
               260                     265                     270

Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys
               275                     280                     285

Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp
               290                     295                     300

Lys Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp
               305                     310                     315

Gly Pro Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile
               320                     325                     330
```

<210> 40
<211> 2498

<400> 40
cgtctctgcg ttcgccatgc gtcccggggc gccagggcca ctctggcctc 50

tgccctgggg ggccctggct tgggccgtgg gcttcgtgag ctccatgggc 100

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ggccacctgc agcctggtgc tccagactga tgtcacccgg gccgagtgct 200

gtgcctccgg caacattgac accgcctggt ccaacctcac ccacccgggg 250

aacaagatca acctcctcgg cttcttgggc cttgtccact gccttccctg 300

caaagattcg tgcgacggcg tggagtgcgg cccgggcaag gcgtgccgca 350

tgctgggggg ccgcccgcgc tgcgagtgcg cgcccgactg ctcggggctc 400

ccggcgcggc tgcaggtctg cggctcagac ggcgccacct accgcgacga 450

gtgcgagctg cgcgccgcgc gctgccgcgg ccacccggac ctgagcgtca 500

tgtaccgggg ccgctgccgc aagtcctgtg agcacgtggt gtgcccgcgg 550

ccacagtcgt gcgtcgtgga ccagacgggc agcgcccact gcgtggtgtg 600

tcgagcggcg ccctgccctg tgccctccag ccccggccag gagctttgcg 650

gcaacaacaa cgtcacctac atctcctcgt gccacatgcg ccaggccacc 700

tgcttcctgg gccgctccat cggcgtgcgc cacgcgggca gctgcgcagg 750

cacccctgag gagccgccag gtggtgagtc tgcagaagag gaagagaact 800

tcgtgtgagc ctgcaggaca ggcctgggcc tggtgcccga ggccccccat 850

catcccctgt tatttattgc cacagcagag tctaatttat atgccacgga 900

cactccttag agcccggatt cggaccactt ggggatccca gaacctccct 950

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cacacttccg ctcctttggg gataaaccta ttaattattg ctactatcaa 1150

gagggctggg cattctctgc tggtaattcc tgaagaggca tgactgcttt 1200

tctcagcccc aagcctctag tctgggtgtg tacggagggt ctagcctggg 1250

tgtgtacgga gggtctagcc tgggtgagta cggagggtct agcctgggtg 1300

agtacggagg gtctagcctg ggtgagtacg gagggtctag cctgggtgtg 1350

38

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tatggaggat ctagcctggg tgagtatgga gggtctagcc tgggtgagta 1400

tggagggtct agcctgggtg tgtatggagg gtctagcctg ggtgagtatg 1450

gagggtctag cctgggtgtg tatggagggt ctagcctggg tgagtatgga 1500

gggtctagcc tgggtgtgta cggagggtct agtctgagtg cgtgtgggga 1550

cctcagaaca ctgtgacctt agcccagcaa gccaggccct tcatgaaggc 1600

caagaaggct gccaccattc cctgccagcc aagaactcc agcttcccca 1650

ctgcctctgt gtgccccttt gcgtcctgtg aaggccattg agaaatgccc 1700

agtgtgcccc ctgggaaagg gcacggcctg tgctcctgac acgggctgtg 1750

cttggccaca gaaccaccca gcgtctcccc tgctgctgtc cacgtcagtt 1800

catgaggcaa cgtcgcgtgg tctcagacgt ggagcagcca gcggcagctc 1850

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gggctccttg gtcccccaca acctgccccg gccaggcctg cagacccaga 2100

ctccagccag acctgcctca cccaccaatg cagccggggc tggcgacacc 2150

agccaggtgc tggtcttggg ccagttctcc cacgacggct caccctcccc 2200

tccatctgcg ttgatgctca gaatcgccta cctgtgcctg cgtgtaaacc 2250

acagcctcag accagctatg gggagaggac aacacggagg atatccagct 2300

tccccggtct ggggtgagga atgtggggag cttgggcatc ctcctccagc 2350

ctcctccagc ccccaggcag tgccttacct gtggtgccca gaaaagtgcc 2400

cctaggttgg tgggtctaca ggagcctcag ccaggcagcc caccccaccc 2450

tggggccctg cctcaccaag gaaataaaga ctcaagccat aaaaaaaa 2498
```

<210> 41
<211> 263
<212> PRT
<213> Homo Sapien

<400> 41
```
Met Arg Pro Gly Ala Pro Gly Pro Leu Trp Pro Leu Pro Trp Gly
 1               5                  10                  15

Ala Leu Ala Trp Ala Val Gly Phe Val Ser Ser Met Gly Ser Gly
              20                  25                  30
```

```
Asn Pro Ala Pro Gly Gly Val Cys Trp Leu Gln Gln Gly Gln Glu
                  35              40                          45

Ala Thr Cys Ser Leu Val Leu Gln Thr Asp Val Thr Arg Ala Glu
                  50              55                          60

Cys Cys Ala Ser Gly Asn Ile Asp Thr Ala Trp Ser Asn Leu Thr
                  65              70                          75

His Pro Gly Asn Lys Ile Asn Leu Leu Gly Phe Leu Gly Leu Val
                  80              85                          90

His Cys Leu Pro Cys Lys Asp Ser Cys Asp Gly Val Glu Cys Gly
                  95              100                        105

Pro Gly Lys Ala Cys Arg Met Leu Gly Gly Arg Pro Arg Cys Glu
                  110             115                        120

Cys Ala Pro Asp Cys Ser Gly Leu Pro Ala Arg Leu Gln Val Cys
                  125             130                        135

Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu Cys Glu Leu Arg Ala
                  140             145                        150

Ala Arg Cys Arg Gly His Pro Asp Leu Ser Val Met Tyr Arg Gly
                  155             160                        165

Arg Cys Arg Lys Ser Cys Glu His Val Val Cys Pro Arg Pro Gln
                  170             175                        180

Ser Cys Val Val Asp Gln Thr Gly Ser Ala His Cys Val Val Cys
                  185             190                        195

Arg Ala Ala Pro Cys Pro Val Pro Ser Ser Pro Gly Gln Glu Leu
                  200             205                        210

Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Met Arg
                  215             220                        225

Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Ala
                  230             235                        240

Gly Ser Cys Ala Gly Thr Pro Glu Glu Pro Pro Gly Gly Glu Ser
                  245             250                        255

Ala Glu Glu Glu Glu Asn Phe Val
                  260
```

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
tcctgtgagc acgtggtgtg 20

40

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
 gggtgggata gacctgcg 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
 aaggccaaga aggctgcc 18

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
 ccaggcctgc agacccag 18

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
 cttcctcagt ccttccagga tatc 24

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
 aagctggata tcctccgtgt tgtc 24

<210> 48
<211> 27
<212> DNA

41

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
 cctgaagagg catgactgct tttctca 27

<210> 49
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
 ggggataaac ctattaatta ttgctac 27

<210> 50
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
 aacgtcacct acatctcctc gtgccacatg cgccaggcca cctg 44

<210> 51
<211> 1690
<212> DNA
<213> Homo Sapien

<400> 51
 tgcagagctt gtggaggcca tggggcgcgt cgtcgcggag ctcgtctcct 50

 cgctgctggg gttgtggctg ttgctgtgca gctgcggatg ccccgagggc 100

 gccgagctgc gtgctccgcc agataaaatc gcgattattg gagccggaat 150

 tggtggcact tcagcagcct attacctgcg gcagaaattt gggaaagatg 200

 tgaagataga cctgtttgaa agagaagagg tcgggggccg cctggctacc 250

 atgatggtgc aggggcaaga atacgaggca ggaggttctg tcatccatcc 300

 tttaaatctg cacatgaaac gttttgtcaa agacctgggt ctctctgctg 350

 ttcaggcctc tggtggccta ctggggatat ataatggaga gactctggta 400

 tttgaggaga gcaactggtt cataattaac gtgattaaat tagtttggcg 450

 ctatggattt caatccctcc gtatgcacat gtgggtagag gacgtgttag 500

 acaagttcat gaggatctac cgctaccagt ctcatgacta tgccttcagt 550

42

```
agtgtcgaaa aattacttca tgctctagga ggagatgact tccttggaat 600

gcttaatcga acacttcttg aaaccttgca aaaggccggc ttttctgaga 650

agttcctcaa tgaaatgatt gctcctgtta tgagggtcaa ttatggccaa 700

agcacggaca tcaatgcctt tgtgggggcg gtgtcactgt cctgttctga 750

ttctggcctt tgggcagtag aaggtggcaa taaacttgtt tgctcagggc 800

ttctgcaggc atccaaaagc aatcttatat ctggctcagt aatgtacatc 850

gaggagaaaa caaagaccaa gtacacagga aatccaacaa agatgtatga 900

agtggtctac caaattggaa ctgagactcg ttcagacttc tatgacatcg 950

tcttggtggc cactccgttg aatcgaaaaa tgtcgaatat tacttttctc 1000

aactttgatc ctccaattga ggaattccat caatattatc aacatatagt 1050

gacaacttta gttaaggggg aattgaatac atctatcttt agctctagac 1100

ccatagataa atttggcctt aatacagttt taaccactga taattcagat 1150

ttgttcatta acagtattgg gattgtgccc tctgtgagag aaaaggaaga 1200

tcctgagcca tcaacagatg gaacatatgt ttggaagatc ttttcccaag 1250

aaactcttac taaagcacaa attttaaagc tctttctgtc ctatgattat 1300

gctgtgaaga agccatggct tgcatatcct cactataagc ccccggagaa 1350

atgcccctct atcattctcc atgatcgact ttattacctc aatggcatag 1400

agtgtgcagc aagtgccatg gagatgagtg ccattgcagc ccacaacgct 1450

gcactccttg cctatcaccg ctggaacggg cacacagaca tgattgatca 1500

ggatggctta tatgagaaac ttaaaactga actatgaagt gacacactcc 1550

tttttcccct cctagttcca aatgactatc agtggcaaaa aagaacaaaa 1600

tctgagcaga gatgattttg aaccagatat tttgccatta tcattgttta 1650

ataaaagtaa tccctgctgg tcataggaaa aaaaaaaaaa 1690
```

<210> 52
<211> 505
<212> PRT
<213> Homo Sapien

<400> 52
```
Met Gly Arg Val Val Ala Glu Leu Val Ser Ser Leu Leu Gly Leu
 1               5                  10                      15

Trp Leu Leu Leu Cys Ser Cys Gly Cys Pro Glu Gly Ala Glu Leu
                20                  25                      30
```

```
Arg Ala Pro Pro Asp Lys Ile Ala Ile Ile Gly Ala Gly Ile Gly
              35              40                      45

Gly Thr Ser Ala Ala Tyr Tyr Leu Arg Gln Lys Phe Gly Lys Asp
              50              55                      60

Val Lys Ile Asp Leu Phe Glu Arg Glu Glu Val Gly Gly Arg Leu
              65              70                      75

Ala Thr Met Met Val Gln Gly Gln Glu Tyr Glu Ala Gly Gly Ser
              80              85                      90

Val Ile His Pro Leu Asn Leu His Met Lys Arg Phe Val Lys Asp
              95              100                     105

Leu Gly Leu Ser Ala Val Gln Ala Ser Gly Gly Leu Leu Gly Ile
              110             115                     120

Tyr Asn Gly Glu Thr Leu Val Phe Glu Glu Ser Asn Trp Phe Ile
              125             130                     135

Ile Asn Val Ile Lys Leu Val Trp Arg Tyr Gly Phe Gln Ser Leu
              140             145                     150

Arg Met His Met Trp Val Glu Asp Val Leu Asp Lys Phe Met Arg
              155             160                     165

Ile Tyr Arg Tyr Gln Ser His Asp Tyr Ala Phe Ser Ser Val Glu
              170             175                     180

Lys Leu Leu His Ala Leu Gly Gly Asp Asp Phe Leu Gly Met Leu
              185             190                     195

Asn Arg Thr Leu Leu Glu Thr Leu Gln Lys Ala Gly Phe Ser Glu
              200             205                     210

Lys Phe Leu Asn Glu Met Ile Ala Pro Val Met Arg Val Asn Tyr
              215             220                     225

Gly Gln Ser Thr Asp Ile Asn Ala Phe Val Gly Ala Val Ser Leu
              230             235                     240

Ser Cys Ser Asp Ser Gly Leu Trp Ala Val Glu Gly Gly Asn Lys
              245             250                     255

Leu Val Cys Ser Gly Leu Leu Gln Ala Ser Lys Ser Asn Leu Ile
              260             265                     270

Ser Gly Ser Val Met Tyr Ile Glu Glu Lys Thr Lys Thr Lys Tyr
              275             280                     285

Thr Gly Asn Pro Thr Lys Met Tyr Glu Val Val Tyr Gln Ile Gly
              290             295                     300

Thr Glu Thr Arg Ser Asp Phe Tyr Asp Ile Val Leu Val Ala Thr
              305             310                     315

Pro Leu Asn Arg Lys Met Ser Asn Ile Thr Phe Leu Asn Phe Asp
```

44

```
                320                      325                      330
Pro Pro Ile Glu Glu Phe His Gln Tyr Tyr Gln His Ile Val Thr
            335                      340                      345
Thr Leu Val Lys Gly Glu Leu Asn Thr Ser Ile Phe Ser Ser Arg
            350                      355                      360
Pro Ile Asp Lys Phe Gly Leu Asn Thr Val Leu Thr Thr Asp Asn
            365                      370                      375
Ser Asp Leu Phe Ile Asn Ser Ile Gly Ile Val Pro Ser Val Arg
            380                      385                      390
Glu Lys Glu Asp Pro Glu Pro Ser Thr Asp Gly Thr Tyr Val Trp
            395                      400                      405
Lys Ile Phe Ser Gln Glu Thr Leu Thr Lys Ala Gln Ile Leu Lys
            410                      415                      420
Leu Phe Leu Ser Tyr Asp Tyr Ala Val Lys Lys Pro Trp Leu Ala
            425                      430                      435
Tyr Pro His Tyr Lys Pro Pro Glu Lys Cys Pro Ser Ile Ile Leu
            440                      445                      450
His Asp Arg Leu Tyr Tyr Leu Asn Gly Ile Glu Cys Ala Ala Ser
            455                      460                      465
Ala Met Glu Met Ser.Ala Ile Ala Ala His Asn Ala Ala Leu Leu
            470                      475                      480
Ala Tyr His Arg Trp Asn Gly His Thr Asp Met Ile Asp Gln Asp
            485                      490                      495
Gly Leu Tyr Glu Lys Leu Lys Thr Glu Leu
            500                      505
```

<210> 53
<211> 728
<212> DNA
<213> Homo Sapien

<400> 53
```
catttccaac aagagcactg gccaagtcag cttcttctga gagagtctct 50

agaagacatg atgctacact cagctttggg tctctgcctc ttactcgtca 100

cagtttcttc caaccttgcc attgcaataa aaaaggaaaa gaggcctcct 150

cagacactct caagaggatg gggagatgac atcacttggg tacaaactta 200

tgaagaaggt ctcttttatg ctcaaaaaag taagaagcca ttaatggtta 250

ttcatcacct ggaggattgt caatactctc aagcactaaa gaaagtattt 300

gcccaaaatg aagaaataca agaaatggct cagaataagt tcatcatgct 350
```

45

```
aaaccttatg catgaaacca ctgataagaa tttatcacct gatgggcaat 400

atgtgcctag aatcatgttt gtagaccctt ctttaacagt tagagctgac 450

atagctggaa gatactctaa cagattgtac acatatgagc ctcgggattt 500

acccctattg atagaaaaca tgaagaaagc attaagactt attcagtcag 550

agctataaga gatgatggaa aaaagccttc acttcaaaga agtcaaattt 600

catgaagaaa acctctggca cattgacaaa tactaaatgt gcaagtatat 650

agattttgta atattactat ttagtttttt taatgtgttt gcaatagtct 700

tattaaaata aatgtttttt aaatctga 728
```

<210> 54
<211> 166
<212> PRT
<213> Homo Sapien

<400> 54

```
Met Met Leu His Ser Ala Leu Gly Leu Cys Leu Leu Leu Val Thr
  1               5                  10                  15

Val Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro
                 20                  25                  30

Pro Gln Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val
                 35                  40                  45

Gln Thr Tyr Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys
                 50                  55                  60

Pro Leu Met Val Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln
                 65                  70                  75

Ala Leu Lys Lys Val Phe Ala Gln Asn Glu Glu Ile Gln Glu Met
                 80                  85                  90

Ala Gln Asn Lys Phe Ile Met Leu Asn Leu Met His Glu Thr Thr
                 95                 100                 105

Asp Lys Asn Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile Met
                110                 115                 120

Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Ala Gly Arg
                125                 130                 135

Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu Pro Arg Asp Leu Pro Leu
                140                 145                 150

Leu Ile Glu Asn Met Lys Lys Ala Leu Arg Leu Ile Gln Ser Glu
                155                 160                 165

Leu
```

46

<210> 55
<211> 537
<212> DNA
<213> Homo Sapien

<400> 55
 taaaacagct acaatattcc agggccagtc acttgccatt tctcataaca 50

 gcgtcagaga aaagaactg actgaaacgt ttgagatgaa gaaagttctc 100

 ctcctgatca cagccatctt ggcagtggct gttggtttcc cagtctctca 150

 agaccaggaa cgagaaaaaa gaagtatcag tgacagcgat gaattagctt 200

 cagggttttt tgtgttccct tacccatatc catttcgccc acttccacca 250

 attccatttc caagatttcc atggtttaga cgtaattttc ctattccaat 300

 acctgaatct gcccctacaa ctccccttcc tagcgaaaag taaacaagaa 350

 ggataagtca cgataaacct ggtcacctga aattgaaatt gagccacttc 400

 cttgaagaat caaaattcct gttaataaaa gaaaaacaaa tgtaattgaa 450

 atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa 500

 acatgaaagc aaagattttg gtttcttaat ttccaca 537

<210> 56
<211> 85
<212> PRT
<213> Homo Sapien

<400> 56
```
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala
 1               5                   10                  15

Val Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser
                20                  25                  30

Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro
                35                  40                  45

Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg
                50                  55                  60

Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser
                65                  70                  75

Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
                80                  85
```

<210> 57
<211> 2997
<212> DNA
<213> Homo Sapien

<400> 57

```
cggacgcgtg ggcgggcgcg ccgggaggga ccggcggcgg catgggccgg 50

gggccctggg atgcgggccc gtctcgccgc ctgctgccgc tgttgctgct 100

gctcggcctg gcccgcggcg ccgcgggagc gccgggcccc gacggtttag 150

acgtctgtgc cacttgccat gaacatgcca catgccagca aagagaaggg 200

aagaagatct gtatttgcaa ctatggattt gtagggaacg ggaggactca 250

gtgtgttgat aaaaatgagt gccagtttgg agccactctt gtctgtggga 300

accacacatc ttgccacaac accccCgggg gcttctattg catttgcctg 350

gaaggatatc gagccacaaa caacaacaag acattcattc ccaacgatgg 400

cacctttgt acagacatag atgagtgtga agtttctggc ctgtgcaggc 450

atggagggcg atgcgtgaac actcatggga gctttgaatg ctactgtatg 500

gatggatact tgccaaggaa tggacctgaa cctttccacc cgaccaccga 550

tgccacatca tgcacagaaa tagactgtgg taccCctcct gaggttccag 600

atggctatat cataggaaat tatacgtcta gtctgggcag ccaggttcgt 650

tatgcttgca gagaaggatt cttcagtgtt ccagaagata cagtttcaag 700

ctgcacaggc ctgggcacat gggagtcccc aaaattacat tgccaagaga 750

tcaactgtgg caaccctcca gaaatgcggc acgccatctt ggtaggaaat 800

cacagctcca ggctgggcgg tgtggctcgc tatgtctgtc aagagggctt 850

tgagagccct ggaggaaaga tcacttctgt ttgcacagag aaaggcacct 900

ggagagaaag tactttaaca tgcacagaaa ttctgacaaa gattaatgat 950

gtatcactgt ttaatgatac ctgtgtgaga tggcaaataa actcaagaag 1000

aataaacccc aagatctcat atgtgatatc cataaaagga caacggttgg 1050

accctatgga atcagttcgt gaggagacag tcaacttgac cacagacagc 1100

aggaccccag aagtgtgcct agccctgtac ccaggcacca actacaccgt 1150

gaacatctcc acagcacctc ccaggcgctc gatgccagcc gtcatcggtt 1200

tccagacagc tgaagttgat ctcttagaag atgatggaag tttcaatatt 1250

tcaatattta atgaaacttg tttgaaattg aacaggcgtt ctaggaaagt 1300

tggatcagaa cacatgtacc aatttaccgt tctgggtcag aggtggtatc 1350

tggctaactt ttctcatgca acatcgttta acttcacaac gagggaacaa 1400

gtgcctgtag tgtgtttgga tctgtaccct acgactgatt atacggtgaa 1450
```

48

```
tgtgaccctg ctgagatctc ctaagcggca ctcagtgcaa ataacaatag 1500

caactccccc agcagtaaaa cagaccatca gtaacatttc aggatttaat 1550

gaaacctgct tgagatggag aagcatcaag acagctgata tggaggagat 1600

gtatttattc cacatttggg gccagagatg gtatcagaag gaatttgccc 1650

aggaaatgac ctttaatatc agtagcagca gccgagatcc cgaggtgtgc 1700

ttggacctac gtccgggtac caactacaat gtcagtctcc gggctctgtc 1750

ttcggaactt cctgtggtca tctccctgac aacccagata acagagcctc 1800

ccctcccgga agtagaattt tttacggtgc acagaggacc tctaccacgc 1850

ctcagactga ggaaagccaa ggagaaaaat ggaccaatca gttcatatca 1900

ggtgttagtg cttcccctgg ccctccaaag cacattttct tgtgattctg 1950

aaggcgcttc ctccttcttt agcaacgcct ctgatgctga tggatacgtg 2000

gctgcagaac tactggccaa agatgttcca gatgatgcca tggagatacc 2050

tataggagac aggctgtact atggggaata ttataatgca cccttgaaaa 2100

gagggagtga ttactgcatt atattacgaa tcacaagtga atggaataag 2150

gtgagaagac actcctgtgc agtttgggct caggtgaaag attcgtcact 2200

catgctgctg cagatggcgg gtgttggact gggttccctg gctgttgtga 2250

tcattctcac attcctctcc ttctcagcgg tgtgatggca gatggacact 2300

gagtggggag gatgcactgc tgctgggcag gtgttctggc agcttctcag 2350

gtgcccgcac agaggctccg tgtgacttcc gtccagggag catgtgggcc 2400

tgcaactttc tccattccca gctgggcccc attcctggat ttaagatggt 2450

ggctatccct gaggagtcac cataaggaga aaactcagga attctgagtc 2500

ttccctgcta caggaccagt tctgtgcaat gaacttgaga ctcctgatgt 2550

acactgtgat attgaccgaa ggctacatac agatctgtga atcttggctg 2600

ggacttcctc tgagtgatgc ctgagggtca gctcctctag acattgactg 2650

caagagaatc tctgcaacct cctatataaa agcatttctg ttaattcatt 2700

cagaatccat tctttacaat atgcagtgag atgggcttaa gtttgggcta 2750

gagtttgact ttatgaagga ggtcattgaa aaagagaaca gtgacgtagg 2800

caaatgtttc aagcacttta gaaacagtac ttttcctata attagttgat 2850

atactaatga gaaaatatac tagcctggcc atgccaataa gtttcctgct 2900
```

49

gtgtctgtta ggcagcattg ctttgatgca atttctattg tcctatatat 2950

tcaaaagtaa tgtctacatt ccagtaaaaa tatcccgtaa ttaaaaa 2997

<210> 58
<211> 747
<212> PRT
<213> Homo Sapien

<400> 58

```
Met Gly Arg Gly Pro Trp Asp Ala Gly Pro Ser Arg Arg Leu Leu
 1               5                  10                  15

Pro Leu Leu Leu Leu Leu Gly Leu Ala Arg Gly Ala Ala Gly Ala
                20                  25                  30

Pro Gly Pro Asp Gly Leu Asp Val Cys Ala Thr Cys His Glu His
                35                  40                  45

Ala Thr Cys Gln Gln Arg Glu Gly Lys Lys Ile Cys Ile Cys Asn
                50                  55                  60

Tyr Gly Phe Val Gly Asn Gly Arg Thr Gln Cys Val Asp Lys Asn
                65                  70                  75

Glu Cys Gln Phe Gly Ala Thr Leu Val Cys Gly Asn His Thr Ser
                80                  85                  90

Cys His Asn Thr Pro Gly Gly Phe Tyr Cys Ile Cys Leu Glu Gly
                95                  100                 105

Tyr Arg Ala Thr Asn Asn Asn Lys Thr Phe Ile Pro Asn Asp Gly
                110                 115                 120

Thr Phe Cys Thr Asp Ile Asp Glu Cys Glu Val Ser Gly Leu Cys
                125                 130                 135

Arg His Gly Gly Arg Cys Val Asn Thr His Gly Ser Phe Glu Cys
                140                 145                 150

Tyr Cys Met Asp Gly Tyr Leu Pro Arg Asn Gly Pro Glu Pro Phe
                155                 160                 165

His Pro Thr Thr Asp Ala Thr Ser Cys Thr Glu Ile Asp Cys Gly
                170                 175                 180

Thr Pro Pro Glu Val Pro Asp Gly Tyr Ile Ile Gly Asn Tyr Thr
                185                 190                 195

Ser Ser Leu Gly Ser Gln Val Arg Tyr Ala Cys Arg Glu Gly Phe
                200                 205                 210

Phe Ser Val Pro Glu Asp Thr Val Ser Ser Cys Thr Gly Leu Gly
                215                 220                 225

Thr Trp Glu Ser Pro Lys Leu His Cys Gln Glu Ile Asn Cys Gly
                230                 235                 240
```

50

```
Asn Pro Pro Glu Met Arg His Ala Ile Leu Val Gly Asn His Ser
                245                 250                 255

Ser Arg Leu Gly Gly Val Ala Arg Tyr Val Cys Gln Glu Gly Phe
                260                 265                 270

Glu Ser Pro Gly Gly Lys Ile Thr Ser Val Cys Thr Glu Lys Gly
                275                 280                 285

Thr Trp Arg Glu Ser Thr Leu Thr Cys Thr Glu Ile Leu Thr Lys
                290                 295                 300

Ile Asn Asp Val Ser Leu Phe Asn Asp Thr Cys Val Arg Trp Gln
                305                 310                 315

Ile Asn Ser Arg Arg Ile Asn Pro Lys Ile Ser Tyr Val Ile Ser
                320                 325                 330

Ile Lys Gly Gln Arg Leu Asp Pro Met Glu Ser Val Arg Glu Glu
                335                 340                 345

Thr Val Asn Leu Thr Thr Asp Ser Arg Thr Pro Glu Val Cys Leu
                350                 355                 360

Ala Leu Tyr Pro Gly Thr Asn Tyr Thr Val Asn Ile Ser Thr Ala
                365                 370                 375

Pro Pro Arg Arg Ser Met Pro Ala Val Ile Gly Phe Gln Thr Ala
                380                 385                 390

Glu Val Asp Leu Leu Glu Asp Asp Gly Ser Phe Asn Ile Ser Ile
                395                 400                 405

Phe Asn Glu Thr Cys Leu Lys Leu Asn Arg Arg Ser Arg Lys Val
                410                 415                 420

Gly Ser Glu His Met Tyr Gln Phe Thr Val Leu Gly Gln Arg Trp
                425                 430                 435

Tyr Leu Ala Asn Phe Ser His Ala Thr Ser Phe Asn Phe Thr Thr
                440                 445                 450

Arg Glu Gln Val Pro Val Val Cys Leu Asp Leu Tyr Pro Thr Thr
                455                 460                 465

Asp Tyr Thr Val Asn Val Thr Leu Leu Arg Ser Pro Lys Arg His
                470                 475                 480

Ser Val Gln Ile Thr Ile Ala Thr Pro Pro Ala Val Lys Gln Thr
                485                 490                 495

Ile Ser Asn Ile Ser Gly Phe Asn Glu Thr Cys Leu Arg Trp Arg
                500                 505                 510

Ser Ile Lys Thr Ala Asp Met Glu Glu Met Tyr Leu Phe His Ile
                515                 520                 525

Trp Gly Gln Arg Trp Tyr Gln Lys Glu Phe Ala Gln Glu Met Thr
```

51

```
                   530                    535                    540
Phe Asn Ile Ser Ser Ser Ser Arg Asp Pro Glu Val Cys Leu Asp
                545                    550                    555
Leu Arg Pro Gly Thr Asn Tyr Asn Val Ser Leu Arg Ala Leu Ser
                560                    565                    570
Ser Glu Leu Pro Val Val Ile Ser Leu Thr Thr Gln Ile Thr Glu
                575                    580                    585
Pro Pro Leu Pro Glu Val Glu Phe Phe Thr Val His Arg Gly Pro
                590                    595                    600
Leu Pro Arg Leu Arg Leu Arg Lys Ala Lys Glu Lys Asn Gly Pro
                605                    610                    615
Ile Ser Ser Tyr Gln Val Leu Val Leu Pro Leu Ala Leu Gln Ser
                620                    625                    630
Thr Phe Ser Cys Asp Ser Glu Gly Ala Ser Ser Phe Phe Ser Asn
                635                    640                    645
Ala Ser Asp Ala Asp Gly Tyr Val Ala Ala Glu Leu Leu Ala Lys
                650                    655                    660
Asp Val Pro Asp Asp Ala Met Glu Ile Pro Ile Gly Asp Arg Leu
                665                    670                    675
Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro Leu Lys Arg Gly Ser Asp
                680                    685                    690
Tyr Cys Ile Ile Leu Arg Ile Thr Ser Glu Trp Asn Lys Val Arg
                695                    700                    705
Arg His Ser Cys Ala Val Trp Ala Gln Val Lys Asp Ser Ser Leu
                710                    715                    720
Met Leu Leu Gln Met Ala Gly Val Gly Leu Gly Ser Leu Ala Val
                725                    730                    735
Val Ile Ile Leu Thr Phe Leu Ser Phe Ser Ala Val
                740                    745
```

<210> 59
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
 ccacttgcca tgaacatgcc ac 22

<210> 60
<211> 25
<212> DNA

52

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 60
 cctcttgaca gacatagcga gccac 25

<210> 61
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
 cactcttgtc tgtgggaacc acacatcttg ccacaactgt ggc 43

<210> 62
<211> 2015
<212> DNA
<213> Homo Sapien

<400> 62
 ggaaaaggta cccgcgagag acagccagca gttctgtgga gcagcggtgg 50

 ccggctagga tgggctgtct ctggggtctg gctctgcccc ttttcttctt 100

 ctgctgggag gttggggtct ctgggagctc tgcaggcccc agcacccgca 150

 gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200

 ctagcaccgg gccacgccgc tctggaaact caaacgctga gcgctgagac 250

 ctcttctagg gcctcaaccc cagccggccc cattccagaa gcagagacca 300

 ggggagccaa gagaatttcc cctgcaagag agaccaggag tttcacaaaa 350

 acatctccca acttcatggt gctgatcgcc acctccgtgg agacatcagc 400

 cgccagtggc agccccgagg gagctggaat gaccacagtt cagaccatca 450

 caggcagtga tcccgaggaa gccatctttg acaccctttg caccgatgac 500

 agctctgaag aggcaaagac actcacaatg gacatattga cattggctca 550

 cacctccaca gaagctaagg gcctgtcctc agagagcagt gcctcttccg 600

 acggccccca tccagtcatc accccgtcac gggcctcaga gagcagcgcc 650

 tcttccgacg gcccccatcc agtcatcacc ccgtcacggg cctcagagag 700

 cagcgcctct tccgacggcc cccatccagt catcaccccg tcatggtccc 750

 cgggatctga tgtcactctc ctcgctgaag ccctggtgac tgtcacaaac 800

 atcgaggtta ttaattgcag catcacagaa atagaaacaa caacttccag 850

53

```
catccctggg gcctcagaca tagatctcat ccccacggaa ggggtgaagg 900

cctcgtccac ctccgatcca ccagctctgc ctgactccac tgaagcaaaa 950

ccacacatca ctgaggtcac agcctctgcc gagaccctgt ccacagccgg 1000

caccacagag tcagctgcac ctcatgccac ggttgggacc ccactcccca 1050

ctaacagcgc cacagaaaga gaagtgacag cacccggggc cacgaccctc 1100

agtggagctc tggtcacagt tagcaggaat cccctggaag aaacctcagc 1150

cctctctgtt gagacaccaa gttacgtcaa agtctcagga gcagctccgg 1200

tctccataga ggctgggtca gcagtgggca aaacaacttc ctttgctggg 1250

agctctgctt cctcctacag cccctcggaa gccgccctca agaacttcac 1300

cccttcagag acaccgacca tggacatcgc aaccaagggg cccttcccca 1350

ccagcaggga ccctcttcct tctgtccctc cgactacaac caacagcagc 1400

cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450

gatgaagccc caacagccac gcccacgact gcccggacga ggccgaccac 1500

agacgtgagt gcaggtgaaa atggaggttt cctcctcctg cggctgagtg 1550

tggcttcccc ggaagacctc actgacccca gagtggcaga aaggctgatg 1600

cagcagctcc accgggaact ccacgcccac gcgcctcact tccaggtctc 1650

cttactgcgt gtcaggagag gctaacggac atcagctgca gccaggcatg 1700

tcccgtatgc caaaagaggg tgctgcccct agcctgggcc cccaccgaca 1750

gactgcagct gcgttactgt gctgagaggt acccagaagg ttcccatgaa 1800

gggcagcatg tccaagcccc taaccccaga tgtggcaaca ggaccctcgc 1850

tcacatccac cggagtgtat gtatggggag gggcttcacc tgttcccaga 1900

ggtgtccttg gactcacctt ggcacatgtt ctgtgtttca gtaaagagag 1950

acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcactcagt 2000

gtggcccaaa aaaaa 2015
```

<210> 63
<211> 482
<212> PRT
<213> Homo Sapien

<400> 63

```
Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys
1               5                   10                  15

Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg
```

```
                    20                      25                      30
   Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala
                    35                      40                      45
   Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu
                    50                      55                      60
   Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile
                    65                      70                      75
   Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg
                    80                      85                      90
   Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu
                    95                     100                     105
   Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu
                   110                     115                     120
   Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
                   125                     130                     135
   Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu
                   140                     145                     150
   Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr
                   155                     160                     165
   Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser
                   170                     175                     180
   Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser
                   185                     190                     195
   Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg
                   200                     205                     210
   Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile
                   215                     220                     225
   Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
                   230                     235                     240
   Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile
                   245                     250                     255
   Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp
                   260                     265                     270
   Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser
                   275                     280                     285
   Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile
                   290                     295                     300
   Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr
                   305                     310                     315
```

55

Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro
                320   325   330

Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr
                335   340   345

Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu
                350   355   360

Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val
                365   370   375

Ser Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly
                380   385   390

Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro
                395   400   405

Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr
                410   415   420

Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro
                425   430   435

Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser Ser Arg Gly Thr
                440   445   450

Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr Met
                455   460   465

Lys Pro Gln Gln Pro Arg Pro Arg Leu Pro Gly Arg Gly Arg Pro
                470   475   480

Gln Thr

<210> 64
<211> 1252
<212> DNA
<213> Homo Sapien

<400> 64
 gcctctgaat tgttgggcag tctggcagtg gagctctccc cggtctgaca 50

 gccactccag aggccatgct tcgtttcttg ccagatttgg ctttcagctt 100

 cctgttaatt ctggctttgg gccaggcagt ccaatttcaa gaatatgtct 150

 ttctccaatt tctgggctta dataaggcgc cttcacccca gaagttccaa 200

 cctgtgcctt atatcttgaa gaaaattttc caggatcgcg aggcagcagc 250

 gaccactggg gtctcccgag acttatgcta cgtaaaggag ctgggcgtcc 300

 gcgggaatgt acttcgcttt ctcccagacc aaggtttctt tctttaccca 350

 aagaaaattt cccaagcttc ctcctgcctg cagaagctcc tctactttaa 400

56

```
cctgtctgcc atcaaagaaa gggaacagtt gacattggcc cagctgggcc 450

tggacttggg gcccaattct tactataacc tgggaccaga gctggaactg 500

gctctgttcc tggttcagga gcctcatgtg tggggccaga ccacccctaa 550

gccaggtaaa atgtttgtgt tgcggtcagt cccatggcca caaggtgctg 600

ttcacttcaa cctgctggat gtagctaagg attggaatga caaccccccgg 650

aaaaatttcg ggttattcct ggagatactg gtcaagaag atagagactc 700

aggggtgaat tttcagcctg aagacacctg tgccagacta agatgctccc 750

ttcatgcttc cctgctggtg gtgactctca accctgatca gtgccaccct 800

tctcggaaaa ggagagcagc catccctgtc cccaagcttt cttgtaagaa 850

cctctgccac cgtcaccagc tattcattaa cttccgggac ctgggttggc 900

acaagtggat cattgccccc aaggggttca tggcaaatta ctgccatgga 950

gagtgtccct tctcactgac catctctctc aacagctcca attatgcttt 1000

catgcaagcc ctgatgcatg ccgttgaccc agagatcccc caggctgtgt 1050

gtatccccac caagctgtct cccatttcca tgctctacca ggacaataat 1100

gacaatgtca ttctacgaca ttatgaagac atggtagtcg atgaatgtgg 1150

gtgtgggtag gatgtcagaa atgggaatag aaggagtgtt cttagggtaa 1200

atcttttaat aaaactacct atctggttta tgaccactta gatcgaaatg 1250

tc 1252
```

```
<210> 65
<211> 364
<212> PRT
<213> Homo Sapien

<400> 65
 Met Leu Arg Phe Leu Pro Asp Leu Ala Phe Ser Phe Leu Leu Ile
  1               5              10                  15

 Leu Ala Leu Gly Gln Ala Val Gln Phe Gln Glu Tyr Val Phe Leu
                 20              25                  30

 Gln Phe Leu Gly Leu Asp Lys Ala Pro Ser Pro Gln Lys Phe Gln
                 35              40                  45

 Pro Val Pro Tyr Ile Leu Lys Lys Ile Phe Gln Asp Arg Glu Ala
                 50              55                  60

 Ala Ala Thr Thr Gly Val Ser Arg Asp Leu Cys Tyr Val Lys Glu
                 65              70                  75

 Leu Gly Val Arg Gly Asn Val Leu Arg Phe Leu Pro Asp Gln Gly
```

57

```
              80                    85                    90
Phe Phe Leu Tyr Pro Lys Lys Ile Ser Gln Ala Ser Ser Cys Leu
             95                   100                   105

Gln Lys Leu Leu Tyr Phe Asn Leu Ser Ala Ile Lys Glu Arg Glu
            110                   115                   120

Gln Leu Thr Leu Ala Gln Leu Gly Leu Asp Leu Gly Pro Asn Ser
            125                   130                   135

Tyr Tyr Asn Leu Gly Pro Glu Leu Glu Leu Ala Leu Phe Leu Val
            140                   145                   150

Gln Glu Pro His Val Trp Gly Gln Thr Thr Pro Lys Pro Gly Lys
            155                   160                   165

Met Phe Val Leu Arg Ser Val Pro Trp Pro Gln Gly Ala Val His
            170                   175                   180

Phe Asn Leu Leu Asp Val Ala Lys Asp Trp Asn Asp Asn Pro Arg
            185                   190                   195

Lys Asn Phe Gly Leu Phe Leu Glu Ile Leu Val Lys Glu Asp Arg
            200                   205                   210

Asp Ser Gly Val Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg Leu
            215                   220                   225

Arg Cys Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn Pro
            230                   235                   240

Asp Gln Cys His Pro Ser Arg Lys Arg Arg Ala Ala Ile Pro Val
            245                   250                   255

Pro Lys Leu Ser Cys Lys Asn Leu Cys His Arg His Gln Leu Phe
            260                   265                   270

Ile Asn Phe Arg Asp Leu Gly Trp His Lys Trp Ile Ile Ala Pro
            275                   280                   285

Lys Gly Phe Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser
            290                   295                   300

Leu Thr Ile Ser Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala
            305                   310                   315

Leu Met His Ala Val Asp Pro Glu Ile Pro Gln Ala Val Cys Ile
            320                   325                   330

Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln Asp Asn Asn
            335                   340                   345

Asp Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val Asp Glu
            350                   355                   360

Cys Gly Cys Gly
```

58

<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
 gtctgacagc cactccagag 20

<210> 67
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
 tctccaattt ctgggcttag ataaggcgcc ttcaccccag aagttcc 47

<210> 68
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 68
 gtcccaggtt atagtaagaa ttgg 24

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
 gtgttgcggt cagtcccatg 20

<210> 70
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
 gctgtctccc atttccatgc 20

<210> 71
<211> 24
<212> DNA

59

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
 cgactaccat gtcttcataa tgtc 24

<210> 72
<211> 2849
<212> DNA
<213> Homo Sapien

<400> 72
 cactttctcc ctctcttcct ttactttcga gaaaccgcgc ttccgcttct 50

 ggtcgcagag acctcggaga ccgcgccggg gagacggagg tgctgtgggt 100

 ggggggacc tgtggctgct cgtaccgccc cccaccctcc tcttctgcac 150

 tgccgtcctc cggaagacct tttcccctgc tctgtttcct tcaccgagtc 200

 tgtgcatcgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250

 ctctaggggc ggcgcgggag gagcggccgg cgggacggag ggcccggcag 300

 gaagatgggc tcccgtggac agggactctt gctggcgtac tgcctgctcc 350

 ttgcctttgc ctctggcctg gtcctgagtc gtgtgcccca tgtccagggg 400

 gaacagcagg agtgggaggg gactgaggag ctgccgtcgc ctccggacca 450

 tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500

 aggggctccc tgcttcccgg tgcttgcgct gctgtgaccc cggtacctcc 550

 atgtacccgg cgaccgccgt gccccagatc aacatcacta tcttgaaagg 600

 ggagaagggt gaccgcggag atcgaggcct ccaagggaaa tatggcaaaa 650

 caggctcagc aggggccagg ggccacactg acccaaagg gcagaagggc 700

 tccatggggg cccctgggga gcggtgcaag agccactacg ccgcctttc 750

 ggtgggccgg aagaagccca tgcacagcaa ccactactac cagacggtga 800

 tcttcgacac ggagttcgtg aacctctacg accacttcaa catgttcacc 850

 ggcaagttct actgctacgt gcccggcctc tacttcttca gcctcaacgt 900

 gcacacctgg aaccagaagg agacctacct gcacatcatg aagaacgagg 950

 aggaggtggt gatcttgttc gcgcaggtgg gcgaccgcag catcatgcaa 1000

 agccagagcc tgatgctgga gctgcgagag caggaccagg tgtgggtacg 1050

 cctctacaag ggcgaacgtg agaacgccat cttcagcgag gagctggaca 1100

```
cctacatcac cttcagtggc tacctggtca agcacgccac cgagccctag 1150

ctggccggcc acctcctttc ctctcgccac cttccacccc tgcgctgtgc 1200

tgaccccacc gcctcttccc cgatccctgg actccgactc cctggctttg 1250

gcattcagtg agacgccctg cacacacaga aagccaaagc gatcggtgct 1300

cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350

ggcggggcac ccgcgagaac cctctgggac cttccgcggc cctctctgca 1400

cacatcctca agtgaccccg cacggcgaga cgcgggtggc ggcagggcgt 1450

cccagggtgc ggcaccgcgg ctccagtcct tggaaataat taggcaaatt 1500

ctaaaggtct caaaaggagc aaagtaaacc gtggaggaca aagaaaaggg 1550

ttgttatttt tgtctttcca gccagcctgc tggctcccaa gagagaggcc 1600

ttttcagttg agactctgct taagagaaga tccaaagtta aagctctggg 1650

gtcaggggag gggccggggg caggaaacta cctctggctt aattctttta 1700

agccacgtag gaactttctt gagggatagg tggaccctga catccctgtg 1750

gccttgccca agggctctgc tggtctttct gagtcacagc tgcgaggtga 1800

tggggggctgg ggccccaggc gtcagcctcc cagagggaca gctgagcccc 1850

ctgccttggc tccaggttgg tagaagcagc cgaagggctc ctgacagtgg 1900

ccagggaccc ctgggtcccc caggcctgca gatgtttcta tgaggggcag 1950

agctccttgg tacatccatg tgtggctctg ctccacccct gtgccacccc 2000

agagccctgg ggggtggtct ccatgcctgc caccctggca tcggctttct 2050

gtgccgcctc ccacacaaat cagccccaga aggccccggg gccttggctt 2100

ctgttttta taaaacacct caagcagcac tgcagtctcc catctcctcg 2150

tgggctaagc atcaccgctt ccacgtgtgt tgtgttggtt ggcagcaagg 2200

ctgatccaga ccccttctgc ccccactgcc ctcatccagg cctctgacca 2250

gtagcctgag aggggctttt tctaggcttc agagcagggg agagctggaa 2300

ggggctagaa agctcccgct tgtctgtttc tcaggctcct gtgagcctca 2350

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ggattcactc tcaggagctg ggtggcagga gaggcaatag cccctgtggc 2450

aattgcagga ccagctggag cagggttgcg gtgtctccac ggtgctctcg 2500

ccctgcccat ggccacccca gactctgatc tccaggaacc ccatagcccc 2550
```

61

.

tctccacctc accccatgtt gatgcccagg gtcactcttg ctacccgctg 2600

ggcccccaaa cccccgctgc ctctcttcct tcccccccatc ccccacctgg 2650

ttttgactaa tcctgcttcc ctctctgggc ctggctgccg ggatctgggg 2700

tccctaagtc cctctcttta aagaacttct gcgggtcaga ctctgaagcc 2750

gagttgctgt gggcgtgccc ggaagcagag cgccacactc gctgcttaag 2800

ctcccccagc tctttccaga aaacattaaa ctcagaattg tgttttcaa 2849

<210> 73
<211> 281
<212> PRT
<213> Homo Sapien

<400> 73

```
Met Gly Ser Arg Gly Gln Gly Leu Leu Leu Ala Tyr Cys Leu Leu
 1               5                  10                  15

Leu Ala Phe Ala Ser Gly Leu Val Leu Ser Arg Val Pro His Val
                20                  25                  30

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
                35                  40                  45

Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
                50                  55                  60

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
                65                  70                  75

Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
                80                  85                  90

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
                95                  100                 105

Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly
                110                 115                 120

Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly
                125                 130                 135

Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val
                140                 145                 150

Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val
                155                 160                 165

Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met
                170                 175                 180

Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe
                185                 190                 195

Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His
```

```
                200                    205                    210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val
                215                    220                    225

Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu
                230                    235                    240

Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg
                245                    250                    255

Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe
                260                    265                    270

Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro
                275                    280
```

<210> 74
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 74
 tacaggccca gtcaggacca gggg 24

<210> 75
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 75
 ctgaagaagt agaggccggg cacg 24

<210> 76
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 76
 cccggtgctt gcgctgctgt gaccccggta cctccatgta cccgg 45

<210> 77
<211> 1042
<212> DNA
<213> Homo Sapien

<400> 77
 gaattcggca cgagggaaga agagaaagaa aatctccggg gctgctggga 50

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gcatataaag aagcccctgtg gccttgctgg ttttaccatc cagaccagag 100

tcaggccaca gacggacatg gctgctcaag gctggtccat gctcctgctg 150

gctgtcctta acctaggcat cttcgtccgt ccctgtgaca ctcaagagct 200

acgatgtctg tgtattcagg aacactctga attcattcct ctcaaactca 250

ttaaaaatat aatggtgata ttcgagacca tttactgcaa cagaaaggaa 300

gtgatagcag tcccaaaaaa tgggagtatg atttgtttgg atcctgatgc 350

tccatgggtg aaggctactg ttggcccaat tactaacagg ttcctacctg 400

aggacctcaa acaaaaggaa tttccaccgg caatgaagct tctgtatagt 450

gttgagcatg aaaagcctct atatctttca tttgggagac ctgagaacaa 500

gagaatattt cccttttccaa ttcgggagac ctctagacac tttgctgatt 550

tagctcacaa cagtgatagg aattttctac gggactccag tgaagtcagc 600

ttgacaggca gtgatgccta aaagccactc atgaggcaaa gagtttcaag 650

gaagctctcc tcctggagtt ttggcgttct cattcttata ctctattccc 700

gcgttagtct ggtgtatgga tctatgagct ctcttttaat attttattat 750

aaatgtttta tttacttaac ttcctagtga atgttcacag gtgactgctc 800

ccccatcccc atttcttgat attacatata atggcatcat ataccccttt 850

attgactgac aaactactca gattgcttaa catttgtgc ttcaaagtct 900

tatcccactc cactatgggc tgttacagag tgcatctcgg tgtagagcaa 950

ggctccttgt cttcagtgcc ccagggtgaa atacttcttt gaaaaatttt 1000

cattcatcag aaaatctgaa ataaaaatat gtcttaattg ag 1042
```

<210> 78
<211> 167
<212> PRT
<213> Homo Sapien

<400> 78

```
Met Ala Ala Gln Gly Trp Ser Met Leu Leu Leu Ala Val Leu Asn
 1               5                  10                  15

Leu Gly Ile Phe Val Arg Pro Cys Asp Thr Gln Glu Leu Arg Cys
                20                  25                  30

Leu Cys Ile Gln Glu His Ser Glu Phe Ile Pro Leu Lys Leu Ile
                35                  40                  45

Lys Asn Ile Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys
                50                  55                  60
```

```
Glu Val Ile Ala Val Pro Lys Asn Gly Ser Met Ile Cys Leu Asp
            65                  70                  75

Pro Asp Ala Pro Trp Val Lys Ala Thr Val Gly Pro Ile Thr Asn
            80                  85                  90

Arg Phe Leu Pro Glu Asp Leu Lys Gln Lys Glu Phe Pro Pro Ala
            95                  100                 105

Met Lys Leu Leu Tyr Ser Val Glu His Glu Lys Pro Leu Tyr Leu
            110                 115                 120

Ser Phe Gly Arg Pro Glu Asn Lys Arg Ile Phe Pro Phe Pro Ile
            125                 130                 135

Arg Glu Thr Ser Arg His Phe Ala Asp Leu Ala His Asn Ser Asp
            140                 145                 150

Arg Asn Phe Leu Arg Asp Ser Ser Glu Val Ser Leu Thr Gly Ser
            155                 160                 165

Asp Ala
```

<210> 79
<211> 798
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 794
<223> unknown base

<400> 79
```
cagacatggc tcagtcactg gctctgagcc tccttatcct ggttctggcc 50

tttggcatcc ccaggaccca aggcagtgat ggaggggctc aggactgttg 100

cctcaagtac agccaaagga agattcccgc caaggttgtc cgcagctacc 150

ggaagcagga accaagctta ggctgctcca tcccagctat cctgttcttg 200

ccccgcaagc gctctcaggc agagctatgt gcagacccaa aggagctctg 250

ggtgcagcag ctgatgcagc atctggacaa gacaccatcc ccacagaaac 300

cagcccaggg ctgcaggaag acaggggggg cctccaagac tggcaagaaa 350

ggaaagggct ccaaaggctg caagaggact gagcggtcac agacccctaa 400

agggccatag cccagtgagc agcctggagc cctggagacc ccaccagcct 450

caccagcgct tgaagcctga acccaagatg caagaaggag gctatgctca 500

ggggccctgg agcagccacc ccatgctggc cttgccacac tctttctcct 550

gctttaacca ccccatctgc attcccagct ctaccctgca tggctgagct 600
```

65

```
gcccacagca ggccaggtcc agagagaccg aggagggaga gtctcccagg 650

gagcatgaga ggaggcagca ggactgtccc cttgaaggag aatcatcagg 700

accctggacc tgatacggct ccccagtaca ccccacctct tccttgtaaa 750

tatgatttat acctaactga ataaaaagct gttctgtctt cccnccca 798
```

<210> 80
<211> 134
<212> PRT
<213> Homo Sapien

<400> 80

```
Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
 1               5                  10                  15

Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp
                20                  25                   30

Cys Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val
                35                  40                   45

Arg Ser Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro
                50                  55                   60

Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys
                65                  70                   75

Ala Asp Pro Lys Glu Leu Trp Val Gln Gln Leu Met Gln His Leu
                80                  85                   90

Asp Lys Thr Pro Ser Pro Gln Lys Pro Ala Gln Gly Cys Arg Lys
                95                  100                 105

Asp Arg Gly Ala Ser Lys Thr Gly Lys Lys Gly Lys Gly Ser Lys
                110                 115                 120

Gly Cys Lys Arg Thr Glu Arg Ser Gln Thr Pro Lys Gly Pro
                125                 130
```

<210> 81
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
```
agacatggct cagtcactgg 20
```

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82
 gacccctaaa gggccatag 19

<210> 83
<211> 924
<212> DNA
<213> Homo Sapien

<400> 83
 aaggagcagc ccgcaagcac caagtgagag gcatgaagtt acagtgtgtt 50

 tccctttggc tcctgggtac aatactgata ttgtgctcag tagacaacca 100

 cggtctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150

 gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaaat 200

 gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250

 tgtgtgctgc gtgaccaaga acctcctggc gttctacgtg gacagggtgt 300

 tcaaggatca tcaggagcca aaccccaaaa tcttgagaaa aatcagcagc 350

 attgccaact ctttcctcta catgcagaaa actctgcggc aatgtcagga 400

 acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450

 tccatgacaa ctatgatcag ctggaggtcc acgctgctgc cattaaatcc 500

 ctgggagagc tcgacgtctt tctagcctgg attaataaga atcatgaagt 550

 aatgttctca gcttgatgac aaggaacctg tatagtgatc cagggatgaa 600

 cacccctgt gcggtttact gtgggagaca gcccaccttg aaggggaagg 650

 agatggggaa ggccccttgc agctgaaagt cccactggct ggcctcaggc 700

 tgtcttattc cgcttgaaaa taggcaaaaa gtctactgtg gtatttgtaa 750

 taaactctat ctgctgaaag ggcctgcagg ccatcctggg agtaaagggc 800

 tgccttccca tctaatttat tgtaaagtca tatagtccat gtctgtgatg 850

 tgagccaagt gatatcctgt agtacacatt gtactgagtg gtttttctga 900

 ataaattcca tattttacct atga 924

<210> 84
<211> 177
<212> PRT
<213> Homo Sapien

<400> 84
 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu
  1   5   10   15

```
Ile Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile
                20                  25                      30

Ser Thr Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys
                35                  40                      45

Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu
                50                  55                      60

Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys
                65                  70                      75

Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg Val Phe
                80                  85                      90

Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile Ser
                95                  100                     105

Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
                110                 115                     120

Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn
                125                 130                     135

Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His
                140                 145                     150

Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala
                155                 160                     165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala
                170                 175
```

<210> 85
<211> 2137
<212> DNA
<213> Homo Sapien

<400> 85

```
gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc   50

gaaacccggc cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc  100

tgggcggggt caccccggct gggacaagaa gccgccgcct gcctgcccgg  150

gcccggggag ggggctgggg ctggggccgg aggcggggtg tgagtgggtg  200

tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa tgctcgggtg  250

tcttgggcac ctacccgtgg ggcccgtaag gcgctactat ataaggctgc  300

cggcccggag ccgccgcgcc gtcagagcag gagcgctgcg tccaggatct  350

agggccacga ccatcccaac ccggcactca cagccccgca gcgcatcccg  400

gtcgccgccc agcctcccgc acccccatcg ccggagctgc gccgagagcc  450

ccagggaggt gccatgcgga gcgggtgtgt ggtggtccac gtatggatcc  500
```

68

```
tggccggcct ctggctggcc gtggccgggc gccccctcgc cttctcggac 550

gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600

cctgtacacc tccggccccc acgggctctc cagctgcttc ctgcgcatcc 650

gtgccgacgg cgtcgtggac tgcgcgcggg gccagagcgc gcacagtttg 700

ctggagatca aggcagtcgc tctgcggacc gtggccatca agggcgtgca 750

cagcgtgcgg tacctctgca tgggcgccga cggcaagatg caggggctgc 800

ttcagtactc ggaggaagac tgtgctttcg aggaggagat ccgcccagat 850

ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900

cagtgccaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct 950

ctcatttcct gcccatgctg cccatggtcc cagaggagcc tgaggacctc 1000

aggggccact tggaatctga catgttctct tcgcccctgg agaccgacag 1050

catggaccca tttgggcttg tcaccggact ggaggccgtg aggagtccca 1100

gctttgagaa gtaactgaga ccatgcccgg gcctcttcac tgctgccagg 1150

ggctgtggta cctgcagcgt ggggggacgtg cttctacaag aacagtcctg 1200

agtccacgtt ctgtttagct ttaggaagaa acatctagaa gttgtacata 1250

ttcagagttt tccattggca gtgccagttt ctagccaata gacttgtctg 1300

atcataacat tgtaagcctg tagcttgccc agctgctgcc tgggccccca 1350

ttctgctccc tcgaggttgc tggacaagct gctgcactgt ctcagttctg 1400

cttgaatacc tccatcgatg gggaactcac ttcctttgga aaaattctta 1450

tgtcaagctg aaattctcta attttttctc atcacttccc caggagcagc 1500

cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgta 1550

aaacagcagg taaatttcac tcaaccccat gtgggaattg atctatatct 1600

ctacttccag ggaccatttg cccttcccaa atccctccag gccagaactg 1650

actggagcag gcatggccca ccaggcttca ggagtagggg aagcctggag 1700

ccccactcca gccctgggac aacttgagaa ttccccctga ggccagttct 1750

gtcatggatg ctgtcctgag aataacttgc tgtcccggtg tcacctgctt 1800

ccatctccca gcccaccagc cctctgccca cctcacatgc ctccccatgg 1850

attggggcct cccaggcccc ccaccttatg tcaacctgca cttcttgttc 1900

aaaaatcagg aaaagaaaag atttgaagac cccaagtctt gtcaataact 1950
```

69

tgctgtgtgg aagcagcggg ggaagaccta gaaccctttc cccagcactt 2000

ggttttccaa catgatattt atgagtaatt tattttgata tgtacatctc 2050

ttattttctt acattattta tgcccccaaa ttatatttat gtatgtaagt 2100

gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 86
<211> 216
<212> PRT
<213> Homo Sapien

<400> 86

```
Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly
  1               5                  10                  15

Leu Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala
             20                  25                  30

Gly Pro His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg
             35                  40                  45

His Leu Tyr Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu
             50                  55                  60

Arg Ile Arg Ala Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser
             65                  70                  75

Ala His Ser Leu Leu Glu Ile Lys Ala Val Ala Leu Arg Thr Val
             80                  85                  90

Ala Ile Lys Gly Val His Ser Val Arg Tyr Leu Cys Met Gly Ala
             95                 100                 105

Asp Gly Lys Met Gln Gly Leu Leu Gln Tyr Ser Glu Glu Asp Cys
            110                 115                 120

Ala Phe Glu Glu Glu Ile Arg Pro Asp Gly Tyr Asn Val Tyr Arg
            125                 130                 135

Ser Glu Lys His Arg Leu Pro Val Ser Leu Ser Ser Ala Lys Gln
            140                 145                 150

Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu Pro Leu Ser His Phe
            155                 160                 165

Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro Glu Asp Leu Arg
            170                 175                 180

Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu Glu Thr Asp
            185                 190                 195

Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala Val Arg
            200                 205                 210

Ser Pro Ser Phe Glu Lys
            215
```

70

<210> 87
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
 atccgcccag atggctacaa tgtgta 26

<210> 88
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
 gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta 42

<210> 89
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
 ccagtccggt gacaagccca aa 22

<210> 90
<211> 1857
<212> DNA
<213> Homo Sapien

<400> 90
 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc 50

 gatggggaca aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat 100

 tggcgatcct gttgtgctcc ctggcattgg gcagtgttac agtgcactct 150

 tctgaacctg aagtcagaat tcctgagaat aatcctgtga agttgtcctg 200

 tgcctactcg ggcttttctt ctccccgtgt ggagtggaag tttgaccaag 250

 gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300

 gaggaccggg tgaccttctt gccaactggt atcaccttca gtccgtgac 350

 acgggaagac actgggacat acacttgtat ggtctctgag gaaggcggca 400

 acagctatgg ggaggtcaag gtcaagctca tcgtgcttgt gcctccatcc 450

 aagcctacag ttaacatccc ctcctctgcc accattggga accgggcagt 500

71

```
gctgacatgc tcagaacaag atggttcccc accttctgaa tacacctggt 550

tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600

agcaactctt cctatgtcct gaatcccaca acaggagagc tggtctttga 650

tcccctgtca gcctctgata ctggagaata cagctgtgag gcacggaatg 700

ggtatgggac acccatgact tcaaatgctg tgcgcatgga agctgtggag 750

cggaatgtgg gggtcatcgt ggcagccgtc cttgtaaccc tgattctcct 800

gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg 850

acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900

agtgcccgaa gtgaaggaga attcaaacag acctcgtcat tcctggtgtg 950

agcctggtcg gctcaccgcc tatcatctgc atttgcctta ctcaggtgct 1000

accggactct ggcccctgat gtctgtagtt tcacaggatg ccttatttgt 1050

cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat 1100

gtcagctatg tgccccatcc tccttcatgc cctccctccc tttcctacca 1150

ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200

agggatcagg aaggaatcct gggtatgcca ttgacttccc ttctaagtag 1250

acagcaaaaa tggcgggggt cgcaggaatc tgcactcaac tgcccacctg 1300

gctggcaggg atctttgaat aggtatcttg agcttggttc tgggctcttt 1350

ccttgtgtac tgacgaccag ggccagctgt tctagagcgg gaattagagg 1400

ctagagcggc tgaaatggtt gtttggtgat gacactgggg tccttccatc 1450

tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500

ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt 1550

ggaaaatggg agctcttgtt gtggagagca tagtaaattt tcagagaact 1600

tgaagccaaa aggatttaaa accgctgctc taaagaaaag aaaactggag 1650

gctgggcgca gtggctcacg cctgtaatcc cagaggctga ggcaggcgga 1700

tcacctgagg tcgggagttc gggatcagcc tgaccaacat ggagaaaccc 1750

tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtagtccc 1800

agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa 1850

aaaaaaa 1857
```

<210> 91
<211> 299

72

<212> PRT
<213> Homo Sapien

<400> 91

```
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe
1               5                  10                  15

Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr
                20                  25                  30

Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro
                35                  40                  45

Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
                50                  55                  60

Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr
                65                  70                  75

Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
                80                  85                  90

Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly
                95                  100                 105

Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly
                110                 115                 120

Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro
                125                 130                 135

Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
                140                 145                 150

Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr
                155                 160                 165

Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
                170                 175                 180

Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly
                185                 190                 195

Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
                200                 205                 210

Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn
                215                 220                 225

Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
                230                 235                 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe
                245                 250                 255

Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
                260                 265                 270
```

73

```
Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala
                275                 280                 285

Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
                290                 295
```

<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
 tcgcggagct gtgttctgtt tccc 24

<210> 93
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
 acacctggtt caaagatggg 20

<210> 95
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
 taggaagagt tgctgaaggc acgg 24

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

74

<400> 96
 ttgccttact caggtgctac 20

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 97
 actcagcagt ggtaggaaag 20

<210> 98
<211> 1200
<212> DNA
<213> Homo Sapien

<400> 98
 cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgccca 50

 acctcactct gtgcttacag ctgctgattc tctgctgtca aactcagtac 100

 gtgagggacc agggcgccat gaccgaccag ctgagcaggc ggcagatccg 150

 cgagtaccaa ctctacagca ggaccagtgg caagcacgtg caggtcaccg 200

 ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt tgccaagctc 250

 atagtggaga cggacacgtt tggcagccgg gttcgcatca aggggctga 300

 gagtgagaag tacatctgta tgaacaagag gggcaagctc atcgggaagc 350

 ccagcgggaa gagcaaagac tgcgtgttca cggagatcgt gctggagaac 400

 aactatacgg ccttccagaa cgcccggcac gagggctggt tcatggcctt 450

 cacgcggcag gggcggcccc gccaggcttc ccgcagccgc cagaaccagc 500

 gcgaggccca cttcatcaag cgcctctacc aaggccagct gcccttcccc 550

 aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgcccccac 600

 ccgccggacc aagcgcacac ggcggcccca gcccctcacg tagtctggga 650

 ggcaggggc agcagcccct gggccgcctc cccaccccctt tcccttctta 700

 atccaaggac tgggctgggg tggcgggagg ggagccagat ccccgaggga 750

 ggaccctgag ggccgcgaag catccgagcc cccagctggg aagggcagg 800

 ccggtgcccc aggggcggct ggcacagtgc ccccttcccg gacgggtggc 850

 aggccctgga gaggaactga gtgtcaccct gatctcaggc caccagcctc 900

 tgccggcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg 950

```
aaggccttgc agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc 1000

tcggatctcc ctcagtctgc ccccagcccc caaactcctc ctggctagac 1050

tgtaggaagg gacttttgtt tgtttgtttg tttcaggaaa aaagaaaggg 1100

agagagagga aaatagaggg ttgtccactc ctcacattcc acgacccagg 1150

cctgcacccc acccccaact cccagccccg gaataaaacc attttcctgc 1200
```

<210> 99
<211> 205
<212> PRT
<213> Homo Sapien

<400> 99

```
Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln
 1               5                  10                  15

Leu Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly
                20                  25                  30

Ala Met Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln
                35                  40                  45

Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg
                50                  55                  60

Arg Ile Ser Ala Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu
                65                  70                  75

Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Ile Lys Gly
                80                  85                  90

Ala Glu Ser Glu Lys Tyr Ile Cys Met Asn Lys Arg Gly Lys Leu
                95                  100                 105

Ile Gly Lys Pro Ser Gly Lys Ser Lys Asp Cys Val Phe Thr Glu
                110                 115                 120

Ile Val Leu Glu Asn Asn Tyr Thr Ala Phe Gln Asn Ala Arg His
                125                 130                 135

Glu Gly Trp Phe Met Ala Phe Thr Arg Gln Gly Arg Pro Arg Gln
                140                 145                 150

Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu Ala His Phe Ile Lys
                155                 160                 165

Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn His Ala Glu Lys
                170                 175                 180

Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr Arg Arg Thr
                185                 190                 195

Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
                200                 205
```

76

<210> 100
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 100
 cagtacgtga gggaccaggg cgccatga 28

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 101
 ccggtgacct gcacgtgctt gcca 24

<210> 102
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<220>
<221> unsure
<222> 21
<223> unknown base

<400> 102
 gcggatctgc cgcctgctca nctggtcggt catggcgccc t 41

<210> 103
<211> 1679
<212> DNA
<213> Homo Sapien

<400> 103
 gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

 agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

 caaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

 aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

 tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250

 aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

 gtgcactatt gacaaccggg tcacccgggt ggcctggcta aaccgcagca 350

77

ccatcctcta tgctgggaat gacaagtggt gcctggatcc tcgcgtggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450

tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500

caaagacctc tagggtccac ctcattgtgc aagtatctcc caaaattgta 550

gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600

ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650

ctcccaaagc ggttggcttt gtgagtgaag acgaatactt ggaaattcag 700

ggcatcaccc gggagcagtc aggggactac gagtgcagtg cctccaatga 750

cgtggccgcg cccgtggtac ggagagtaaa ggtcaccgtg aactatccac 800

catacatttc agaagccaag ggtacaggtg tccccgtggg acaaaagggg 850

acactgcagt gtgaagcctc agcagtcccc tcagcagaat tccagtggta 900

caaggatgac aaaagactga ttgaaggaaa gaaagggggtg aaagtggaaa 950

acagaccttt cctctcaaaa ctcatcttct tcaatgtctc tgaacatgac 1000

tatgggaact acacttgcgt ggcctccaac aagctgggcc acaccaatgc 1050

cagcatcatg ctatttggtc caggcgccgt cagcgaggtg agcaacggca 1100

cgtcgaggag ggcaggctgc gtctggctgc tgcctcttct ggtcttgcac 1150

ctgcttctca aattttgatg tgagtgccac ttccccaccc gggaaaggct 1200

gccgccacca ccaccaccaa cacaacagca atggcaacac cgacagcaac 1250

caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300

gaaatttgag ggagggggaac aaagaatact ttggggggaa aagagtttta 1350

aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagtttt 1400

cttttcccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450

gctgcatcgt gcaacctctt tggtgccagt gtgggcaagg gctcagcctc 1500

tctgcccaca gagtgccccc acgtggaaca ttctggagct ggccatccca 1550

aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600

gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650

aaacgtgaaa taaaaagagc aaaaaaaaa 1679

<210> 104
<211> 344
<212> PRT
<213> Homo Sapien

78

<400> 104

```
Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala
1               5                   10                  15

Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro
                20                  25                  30

Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val
                35                  40                  45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp
                50                  55                  60

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu
                65                  70                  75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
                80                  85                  90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
                95                  100                 105

Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
                110                 115                 120

Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
                125                 130                 135

Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly
                140                 145                 150

Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro
                155                 160                 165

Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val
                170                 175                 180

Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
                185                 190                 195

Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
                200                 205                 210

Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
                215                 220                 225

Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
                230                 235                 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp
                245                 250                 255

Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys
                260                 265                 270

Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val
                275                 280                 285
```

```
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
                290             295                 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
                305             310                 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
                320             325                 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
                335             340
```

<210> 105
<211> 1734
<212> DNA
<213> Homo Sapien

<400> 105

```
gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50

gacccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100

gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150

agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200

cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc 250

ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300

ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350

caaagaggcc ggaggggcag ctggctctaa agtcagtgag gcccttggcc 400

aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450

ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500

gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550

acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600

ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650

ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaaac tcagcaggca gctttggaat gaatcctcag 750

ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800

caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850

gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900

ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950

cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
```

```
gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050

agtggtggca gcagtggcaa cagtggtggc agcagaggtg acagcggcag 1100

tgagtcctcc tggggatcca gcaccggctc ctcctccggc aaccacggtg 1150

ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200

gaagcccgcg ggagcgggga atctgggatt cagggcttca gaggacaggg 1250

agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300

gaggctctgg agacaattat cggggggcaag ggtcgagctg gggcagtgga 1350

ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400

tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450

gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500

ccgtgacctc cagacaagga gccaccagat tggatgggag ccccacact 1550

ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600

aaataaacct tagctgcccc acaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734
```

<210> 106
<211> 440
<212> PRT
<213> Homo Sapien

<400> 106

```
Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1               5                  10                   15

Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
             20                  25                   30

Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
             35                  40                   45

Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly
             50                  55                   60

Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr
             65                  70                   75

Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly
             80                  85                   90

Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala
             95                  100                  105

Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val
```

81

```
                    110                      115                      120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
                125                      130                      135

Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
                140                      145                      150

Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
                155                      160                      165

Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
                170                      175                      180

Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
                185                      190                      195

Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
                200                      205                      210

Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
                215                      220                      225

Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
                230                      235                      240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser
                245                      250                      255

Gly Ser Gly Ser Asn Gly Asp Asn Asn Gly Ser Ser Ser Gly
                260                      265                      270

Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser
                275                      280                      285

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser
                290                      295                      300

Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly
                305                      310                      315

Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His
                320                      325                      330

Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly
                335                      340                      345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
                350                      355                      360

Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
                365                      370                      375

Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
                380                      385                      390

Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
                395                      400                      405
```

82

```
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
            410                 415                 420

Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
                425                 430                 435

Ser Ser Arg Ile Pro
                440
```

<210> 107
<211> 918
<212> DNA
<213> Homo Sapien

<400> 107

```
agccaggcag cacatcacag cgggaggagc tgtcccaggt ggcccagctc 50

agcaatggca atggggggtcc ccagagtcat tctgctctgc ctctttgggg 100

ctgcgctctg cctgacaggg tcccaagccc tgcagtgcta cagctttgag 150

cacacctact ttggcccctt tgacctcagg gccatgaagc tgcccagcat 200

ctcctgtcct catgagtgct ttgaggctat cctgtctctg gacaccgggt 250

atcgcgcgcc ggtgaccctg gtgcggaagg gctgctggac cgggcctcct 300

gcgggccaga cgcaatcgaa cccggacgcg ctgccgccag actactcggt 350

ggtgcgcggc tgcacaactg acaaatgcaa cgcccacctc atgactcatg 400

acgccctccc caacctgagc caagcacccg acccgccgac gctcagcggc 450

gccgagtgct acgcctgtat cggggtccac caggatgact gcgctatcgg 500

caggtcccga cgagtccagt gtcaccagga ccagaccgcc tgcttccagg 550

gcagtggcag aatgacagtt ggcaatttct cagtccctgt gtacatcaga 600

acctgccacc ggccctcctg caccaccgag ggcaccacca gccctggac 650

agccatcgac ctccagggct cctgctgtga ggggtacctc tgcaacagga 700

aatccatgac ccagcccttc accagtgctt cagccaccac ccctccccga 750

gcactacagg tcctggccct gctcctccca gtcctcctgc tggtggggct 800

ctcagcatag accgcccctc caggatgctg gggacagggc tcacacacct 850

cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt 900

aaagtaagaa ttgcaaaa 918
```

<210> 108
<211> 251
<212> PRT
<213> Homo Sapien

<400> 108
```
Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly
  1           5                  10                      15

Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser
             20                  25                      30

Phe Glu His Thr Tyr Phe Gly Pro Phe Asp Leu Arg Ala Met Lys
             35                  40                      45

Leu Pro Ser Ile Ser Cys Pro His Glu Cys Phe Glu Ala Ile Leu
             50                  55                      60

Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr Leu Val Arg Lys
             65                  70                      75

Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln Ser Asn Pro
             80                  85                      90

Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys Thr Thr
             95                  100                     105

Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro Asn
            110                  115                     120

Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys
            125                  130                     135

Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg
            140                  145                     150

Ser Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln
            155                  160                     165

Gly Ser Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr
            170                  175                     180

Ile Arg Thr Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr
            185                  190                     195

Ser Pro Trp Thr Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly
            200                  205                     210

Tyr Leu Cys Asn Arg Lys Ser Met Thr Gln Pro Phe Thr Ser Ala
            215                  220                     225

Ser Ala Thr Thr Pro Pro Arg Ala Leu Gln Val Leu Ala Leu Leu
            230                  235                     240

Leu Pro Val Leu Leu Leu Val Gly Leu Ser Ala
            245                  250
```

<210> 109
<211> 1813
<212> DNA
<213> Homo Sapien

<400> 109

```
ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt 50

cgcgcagcct cggcacctgc aggtccgtgc gtcccgcggc tggcgcccct 100

gactccgtcc cggccaggga gggccatgat ttccctcccg gggcccctgg 150

tgaccaactt gctgcggttt ttgttcctgg ggctgagtgc cctcgcgccc 200

ccctcgcggg cccagctgca actgcacttg cccgccaacc ggttgcaggc 250

ggtggaggga ggggaagtgg tgcttccagc gtggtacacc ttgcacgggg 300

aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc 350

aaacagaaag aaaaggagga tcaggtgttg tcctacatca atggggtcac 400

aacaagcaaa cctggagtat ccttggtcta ctccatgccc tcccggaacc 450

tgtccctgcg gctggagggt ctccaggaga aagactctgg cccctacagc 500

tgctccgtga atgtgcaaga caaacaaggc aaatctaggg gccacagcat 550

caaaacctta gaactcaatg tactggttcc tccagctcct ccatcctgcc 600

gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag 650

tctccaagga gtaagcccgc tgtccaatac cagtgggatc ggcagcttcc 700

atccttccag actttctttg caccagcatt agatgtcatc cgtgggtctt 750

taagcctcac caacctttcg tcttccatgg ctggagtcta tgtctgcaag 800

gcccacaatg aggtgggcac tgcccaatgt aatgtgacgc tggaagtgag 850

cacagggcct ggagctgcag tggttgctgg agctgttgtg ggtaccctgg 900

ttggactggg gttgctggct gggctggtcc tcttgtacca ccgccggggc 950

aaggccctgg aggagccagc caatgatatc aaggaggatg ccattgctcc 1000

ccggaccctg ccctggccca agagctcaga cacaatctcc aagaatggga 1050

cccttttcctc tgtcacctcc gcacgagccc tccggccacc ccatggccct 1100

cccaggcctg gtgcattgac ccccacgccc agtctctcca gccaggccct 1150

gccctcacca agactgccca cgacagatgg ggcccaccct caaccaatat 1200

cccccatccc tggtggggtt tcttcctctg gcttgagccg catgggtgct 1250

gtgcctgtga tggtgcctgc ccagagtcaa gctggctctc tggtatgatg 1300

accccaccac tcattggcta aaggatttgg ggtctctcct tcctataagg 1350

gtcacctcta gcacagaggc ctgagtcatg ggaaagagtc acactcctga 1400

cccttagtac tctgcccca cctctctttta ctgtgggaaa accatctcag 1450
```

85

taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500

attgggagga gcctccaccc acccctgact cctccttatg aagccagctg 1550

ctgaaattag ctactcacca agagtgaggg gcagagactt ccagtcactg 1600

agtctcccag gccccccttga tctgtacccc acccctatct aacaccaccc 1650

ttggctccca ctccagctcc ctgtattgat ataacctgtc aggctggctt 1700

ggttaggttt tactggggca gaggataggg aatctcttat taaaactaac 1750

atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800

tttgtatgaa aaa 1813

<210> 110
<211> 390
<212> PRT
<213> Homo Sapien

<400> 110

```
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe
  1               5              10                  15

Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln
               20              25                  30

Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly
               35              40                  45

Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val
               50              55                  60

Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
               65              70                  75

Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly
               80              85                  90

Val Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro
               95             100                 105

Ser Arg Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp
              110             115                 120

Ser Gly Pro Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly
              125             130                 135

Lys Ser Arg Gly His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu
              140             145                 150

Val Pro Pro Ala Pro Pro Ser Cys Arg Leu Gln Gly Val Pro His
              155             160                 165

Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser Pro Arg Ser Lys
              170             175                 180
```

86

```
Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro Ser Phe Gln
                185                 190                 195

Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser Leu Ser
                200                 205                 210

Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys Lys
                215                 220                 225

Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
                230                 235                 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val
                245                 250                 255

Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu
                260                 265                 270

Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile
                275                 280                 285

Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser
                290                 295                 300

Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser
                305                 310                 315

Ala Arg Ala Leu Arg Pro Pro His Gly Pro Pro Arg Pro Gly Ala
                320                 325                 330

Leu Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro
                335                 340                 345

Arg Leu Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro
                350                 355                 360

Ile Pro Gly Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala
                365                 370                 375

Val Pro Val Met Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val
                380                 385                 390
```

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 111
 agggtctcca ggagaaagac tc 22

<210> 112
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 112
 attgtgggcc ttgcagacat agac 24

<210> 113
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 113
 ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 114
<211> 2479
<212> DNA
<213> Homo Sapien

<400> 114
 acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt 50

 ttgcacatgg aggacagcag caaagagggc aacacaggct gataagacca 100

 gagacagcag ggagattatt ttaccatacg ccctcaggac gttccctcta 150

 gctggagttc tggacttcaa cagaacccca tccagtcatt ttgattttgc 200

 tgtttatttt tttttttctt ttcttttttcc caccacattg tattttattt 250

 ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300

 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag 350

 gtgtccaaac tcctggcctg ccctagtgtg tgccgctgcg acaggaactt 400

 tgtctactgt aatgagcgaa gcttgacctc agtgcctctt gggatcccgg 450

 agggcgtaac cgtactctac ctccacaaca accaaattaa taatgctgga 500

 tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg tctacctgta 550

 tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600

 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt 650

 gcccagctct tgaagcttga agagctgcac ctggatgaca actccatatc 700

 cacagtgggg gtggaagacg gggccttccg ggaggctatt agcctcaaat 750

 tgttgttttt gtctaagaat cacctgagca gtgtgcctgt tgggcttcct 800

 gtggacttgc aagagctgag agtggatgaa aatcgaattg ctgtcatatc 850

 cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900

88

ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc 950

accaagctca aggaattttc aattgtacgt aattcgctgt cccaccctcc 1000

tcccgatctc ccaggtacgc atctgatcag gctctatttg caggacaacc 1050

agataaacca cattcctttg acagccttct caaatctgcg taagctggaa 1100

cggctggata tatccaacaa ccaactgcgg atgctgactc aaggggtttt 1150

tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200

tttgtgactg cagtattaaa tgggtcacag aatggctcaa atatatccct 1250

tcatctctca acgtgcgggg tttcatgtgc caaggtcctg aacaagtccg 1300

ggggatggcc gtcagggaat taaatatgaa tcttttgtcc tgtcccacca 1350

cgacccccgg cctgcctctc ttcaccccag ccccaagtac agcttctccg 1400

accactcagc ctcccaccct ctctattcca aaccctagca gaagctacac 1450

gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500

gcagagaaag agtgacccca cctatttctg aacggatcca gctctctatc 1550

cattttgtga atgatacttc cattcaagtc agctggctct ctctcttcac 1600

cgtgatggca tacaaactca catgggtgaa aatgggccac agtttagtag 1650

ggggcatcgt tcaggagcgc atagtcagcg gtgagaagca cacctgagc 1700

ctggttaact tagagccccg atccacctat cggatttgtt tagtgccact 1750

ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800

ccacccatgc ctcctatctg aacaacggca gcaacacagc gtccagccat 1850

gagcagacga cgtcccacag catgggctcc ccctttctgc tggcgggctt 1900

gatcggggc gcggtgatat ttgtgctggt ggtcttgctc agcgtctttt 1950

gctggcatat gcacaaaaag gggcgctaca cctcccagaa gtggaaatac 2000

aaccggggcc ggcggaaaga tgattattgc gaggcaggca ccaagaagga 2050

caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100

ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc 2150

ccaaatgggg gcattaatta cacagactgc catatcccca acaacatgcg 2200

atactgcaac agcagcgtgc cagacctgga gcactgccat acgtgacagc 2250

cagaggccca gcgttatcaa ggcggacaat tagactcttg agaacacact 2300

cgtgtgtgca cataaagaca cgcagattac atttgataaa tgttacacag 2350

89

```
         atgcatttgt gcatttgaat actctgtaat ttatacggtg tactatataa 2400

         tgggatttaa aaaaagtgct atcttttcta tttcaagtta attacaaaca 2450

         gttttgtaac tctttgcttt ttaaatctt 2479
```

<210> 115
<211> 660
<212> PRT
<213> Homo Sapien

<400> 115

```
Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe
 1               5                  10                  15

Leu Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val
                20                  25                  30

Ser Lys Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn
                35                  40                  45

Phe Val Tyr Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly
                50                  55                  60

Ile Pro Glu Gly Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile
            65                  70                  75

Asn Asn Ala Gly Phe Pro Ala Glu Leu His Asn Val Gln Ser Val
                80                  85                  90

His Thr Val Tyr Leu Tyr Gly Asn Gln Leu Asp Glu Phe Pro Met
                95                  100                 105

Asn Leu Pro Lys Asn Val Arg Val Leu His Leu Gln Glu Asn Asn
                110                 115                 120

Ile Gln Thr Ile Ser Arg Ala Ala Leu Ala Gln Leu Leu Lys Leu
                125                 130                 135

Glu Glu Leu His Leu Asp Asp Asn Ser Ile Ser Thr Val Gly Val
                140                 145                 150

Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser Leu Lys Leu Leu Phe
                155                 160                 165

Leu Ser Lys Asn His Leu Ser Ser Val Pro Val Gly Leu Pro Val
                170                 175                 180

Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile Ala Val Ile
                185                 190                 195

Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg Leu Ile
                200                 205                 210

Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly Thr
                215                 220                 225

Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
```

```
              230                    235                    240
Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile
              245                    250                    255

Arg Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr
              260                    265                    270

Ala Phe Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn
              275                    280                    285

Asn Gln Leu Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser
              290                    295                    300

Asn Leu Lys Gln Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp
              305                    310                    315

Cys Ser Ile Lys Trp Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser
              320                    325                    330

Ser Leu Asn Val Arg Gly Phe Met Cys Gln Gly Pro Glu Gln Val
              335                    340                    345

Arg Gly Met Ala Val Arg Glu Leu Asn Met Asn Leu Leu Ser Cys
              350                    355                    360

Pro Thr Thr Thr Pro Gly Leu Pro Leu Phe Thr Pro Ala Pro Ser
              365                    370                    375

Thr Ala Ser Pro Thr Thr Gln Pro Pro Thr Leu Ser Ile Pro Asn
              380                  _  385                    390

Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro Thr Thr Ser Lys Leu
              395                    400                    405

Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg Val Thr Pro Pro
                 -  410                    415                    420

Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val Asn Asp Thr
              425                    430                    435

Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met Ala Tyr
              440                    445                    450

Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly Ile
              455                    460                    465

Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
              470                    475                    480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro
              485                    490                    495

Leu Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser
              500                    505                    510

Glu Ala Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr
              515                    520                    525
```

91

```
Ala Ser Ser His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro
                530                 535                 540

Phe Leu Leu Ala Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu
                545                 550                 555

Val Val Leu Leu Ser Val Phe Cys Trp His Met His Lys Lys Gly
                560                 565                 570

Arg Tyr Thr Ser Gln Lys Trp Lys Tyr Asn Arg Gly Arg Arg Lys
                575                 580                 585

Asp Asp Tyr Cys Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu
                590                 595                 600

Glu Met Thr Glu Thr Ser Phe Gln Ile Val Ser Leu Asn Asn Asp
                605                 610                 615

Gln Leu Leu Lys Gly Asp Phe Arg Leu Gln Pro Ile Tyr Thr Pro
                620                 625                 630

Asn Gly Gly Ile Asn Tyr Thr Asp Cys His Ile Pro Asn Asn Met
                635                 640                 645

Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu His Cys His Thr
                650                 655                 660
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<210> 116
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 116
 cggtctacct gtatggcaac c 21

<210> 117
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 117
 gcaggacaac cagataaacc ac 22

<210> 118
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 118

<210> 119
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 119
 ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 120
<211> 2857
<212> DNA
<213> Homo Sapien

<400> 120
 tgaagagtaa tagttggaat caaaagagtc aacgcaatga actgttattt 50

 actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

 caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

 ttgagagtga agcgtggctg ggtgtggaac caatttttg taccagagga 200

 aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250

 atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300

 acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350

 tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400

 tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

 tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500

 cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550

 caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600

 agcttacttc aaggccagcc atattttct gttgaaccaa caacaggagt 650

 cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700

 taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750

 acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800

 atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850

 ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900

 gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950

 tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaag 1000

tggattttga .gcaccagaac cactacggta ttagagcaaa agttaaaaac 1050

catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100

tttcattaag atccaggtgg aagatgttga tgagcctcct cttttcctcc 1150

ttccatatta tgtatttgaa gtttttgaag aaaccccaca gggatcattt 1200

gtaggcgtgg tgtctgccac agacccagac aataggaaat ctcctatcag 1250

gtattctatt actaggagca aagtgttcaa tatcaatgat aatggtacaa 1300

tcactacaag taactcactg gatcgtgaaa tcagtgcttg gtacaaccta 1350

agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400

actgtatgtg caagttctta acatcaatga tcatgctcct gagttctctc 1450

aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500

cagactatca gtgcagtgga tagagatgaa tccatagaag agcaccattt 1550

ttactttaat ctatctgtag aagacactaa caattcaagt tttacaatca 1600

tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650

aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700

tggaatcccg tcacttacaa gtacaaacac ccttaccatc catgtctgtg 1750

actgtggtga cagtgggagc acacagacct gccagtacca ggagcttgtg 1800

cttTccatgg gattcaagac agaagttatc attgctattc tcatttgcat 1850

tatgatcata tttgggttta tttttttgac tttgggttta aaacaacgga 1900

gaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950

ttccaatatg atgatgaagg gggtggagaa gaagatacag aggcctttga 2000

tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050

aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100

ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150

agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200

cttttgaggg aacagggtca ttagctggat ccctgagctc cttagaatca 2250

gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300

tcgctttaaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350

attaggggctt tttaccatca aaatttttaa aagtgctaat gtgtattcga 2400

acccaatggt agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450

94

agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500

ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550

tgtaaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600

aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650

ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700

cgagaaaatt taaaggagca aaaatttgca agtcaaatag aaatgtacaa 2750

atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800

tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850

atttaaa 2857

<210> 121
<211> 772
<212> PRT
<213> Homo Sapien

<400> 121

```
    Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu
    1               5                   10                  15

    Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys
                    20                  25                  30

    Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
                    35                  40                  45

    Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
                    50                  55                  60

    His His Ile Gly Gln, Leu Arg Ser Asp Leu Asp Asn Gly Asn Asn
                    65                  70                  75

    Ser Phe Gln Tyr Lys Leu Leu Gly Ala Gly Ala Gly Ser Thr Phe
                    80                  85                  90

    Ile Ile Asp Glu Arg Thr Gly Asp Ile Tyr Ala Ile Gln Lys Leu
                    95                  100                 105

    Asp Arg Glu Glu Arg Ser Leu Tyr Ile Leu Arg Ala Gln Val Ile
                    110                 115                 120

    Asp Ile Ala Thr Gly Arg Ala Val Glu Pro Glu Ser Glu Phe Val
                    125                 130                 135

    Ile Lys Val Ser Asp Ile Asn Asp Asn Glu Pro Lys Phe Leu Asp
                    140                 145                 150

    Glu Pro Tyr Glu Ala Ile Val Pro Glu Met Ser Pro Glu Gly Thr
                    155                 160                 165

    Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser
```

95

```
                    170                 175                 180
Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro
                    185                 190                 195
Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser
                    200                 205                 210
Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln
                    215                 220                 225
Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr
                    230                 235                 240
Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile
                    245                 250                 255
Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro
                    260                 265                 270
Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile
                    275                 280                 285
Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser
                    290                 295                 300
Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile
                    305                 310                 315
Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr
                    320                 325                 330
Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu
                    335                 340                 345
Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln
                    350                 355                 360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr
                    365                 370                 375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly
                    380                 385                 390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg
                    395                 400                 405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly
                    410                 415                 420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp
                    425                 430                 435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln
                    440                 445                 450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp
                    455                 460                 465
```

96

```
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu
                470             475                 480

Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp
                485             490                 495

Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser
                500             505                 510

Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln
                515             520                 525

Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu
                530             535                 540

Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn
                545             550                 555

Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val
                560             565                 570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln
                575             580                 585

Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala
                590             595                 600

Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr
                605             610                 615

Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys
                620             625                 630

Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly
                635             640                 645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg
                650             655                 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser
                665             670                 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro
                680             685                 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu
                695             700                 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr
                710             715                 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser
                725             730                 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu
                740             745                 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly
```

97

```
              755                 760                 765
     Ser Ala Val Gln Ser Asn Asn
                         770
```

<210> 122
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 122
  cttgactgtc tctgaatctg caccc 25

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 123
  aagtggtgga agcctccagt gtgg 24

<210> 124
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 124
  ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

  gc 52

<210> 125
<211> 1152
<212> DNA
<213> Homo Sapien

<400> 125
  cttcagaaca ggttctcctt ccccagtcac cagttgctcg agttagaatt 50

  gtctgcaatg gccgccctgc agaaatctgt gagctctttc cttatgggga 100

  ccctggccac cagctgcctc cttctcttgg ccctcttggt acagggagga 150

  gcagctgcgc ccatcagctc ccactgcagg cttgacaagt ccaacttcca 200

  gcagccctat atcaccaacc gcaccttcat gctggctaag gaggctagct 250

  tggctgataa caacacagac gttcgtctca ttggggagaa actgttccac 300

98

ggagtcagta tgagtgagcg ctgctatctg atgaagcagg tgctgaactt 350

caccctтgaa gaagtgctgt ccctcaatc tgataggttc cagccttata 400

tgcaggaggt ggtgcccttc ctggccaggc tcagcaacag gctaagcaca 450

tgtcatattg aaggtgatga cctgcatatc cagaggaatg tgcaaaagct 500

gaaggacaca gtgaaaaagc ttggagagag tggagagatc aaagcaattg 550

gagaactgga tttgctgttt atgtctctga gaaatgcctg catttgacca 600

gagcaaagct gaaaaatgaa taactaaccc cctttccctg ctagaaataa 650

caattagatg ccccaaagcg attttttта accaaaagga agatgggaag 700

ccaaactcca tcatgatggg tggattccaa atgaacccct gcgttagtta 750

caaaggaaac caatgccact tttgtttata agaccagaag gtagactttc 800

taagcataga tatttattga taacatttca ttgtaactgg tgttctatac 850

acagaaaaca atttattttt taaataattg tctttttcca taaaaaagat 900

tactttccat tcctttaggg gaaaaaaccc ctaaatagct tcatgtttcc 950

ataatcagta ctttatattt ataaatgtat ttattattat tataagactg 1000

cattttattt atatcatttt attaatatgg atttatttat agaaacatca 1050

ttcgatattg ctacttgagt gtaaggctaa tattgatatt tatgacaata 1100

attatagagc tataacatgt ttatttgacc tcaataaaca cttggatatc 1150

cc 1152

<210> 126
<211> 179
<212> PRT
<213> Homo Sapien

<400> 126
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr
 1   5   10   15

Leu Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu Val Gln Gly
                20   25   30

Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser
                35   40   45

Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala
                50   55   60

Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
                65   70   75

Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr

```
              80                    85                    90
Leu Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe
                95                   100                   105

Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro
                110                  115                   120

Phe Leu Ala Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu
                125                  130                   135

Gly Asp Asp Leu His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp
                140                  145                   150

Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly
                155                  160                   165

Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Ile
                170                  175
```

<210> 127
<211> 2557
<212> DNA
<213> Homo Sapien

<400> 127

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tgcgagaaag gacgcgcgcc ctgcgtcggg cgaagaaaag aagcaaaact 100

tgtcgggagg gtttcgtcat caacctcctt cccgcaaacc taaacctcct 150

gccggggcca tccctagaca gaggaaagtt cctgcagagc cgaccagccc 200

tagtggatct ggggcaggca gcggcgctgg ctgtggaatt agatctgttt 250

tgaacccagt ggagcgcatc gctggggctc ggaagtcacc gtccgcgggc 300

accgggttgg cgctgcccga gtggaaccga cagtttgcga gcctcggctg 350

caagtggcct ctcctccccg cggttgttgt tcagtgtcgg gtgagggctg 400

cgagtgtggc aagttgcaaa gagagcctca gaggtccgaa gagcgctgcg 450

ctcctactcg cgttcgcttc ttcctcttct cggttcccta ctgtgaaatc 500

gcagcgacat ttacaaaggc ctccgggtcc taccgagacc gatccgcagc 550

gtttggcccg gtcgtgccta ttgcatcggg agcccccgag caccggcgaa 600

atggcgaggt tcccgaaggc cgacctggcc gctgcaggag ttatgttact 650

ttgccacttc ttcacggacc agtttcagtt cgccgatggg aaacccggag 700

accaaatcct tgattggcag tatggagtta ctcaggcctt ccctcacaca 750

gaggaggagg tggaagttga ttcacacgcg tacagccaca ggtggaaaag 800
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aaacttggac tttctcaagg cggtagacac gaaccgagca agcgtcggcc 850

aagactctcc tgagcccaga agcttcacag acctgctgct ggatgatggg 900

caggacaata acactcagat cgaggaggat acagaccaca attactatat 950

atctcgaata tatggtccat ctgattctgc cagccgggat ttatgggtga 1000

acatagacca aatggaaaaa gataaagtga agattcatgg aatattgtcc 1050

aatactcatc ggcaagctgc aagagtgaat ctgtccttcg attttccatt 1100

ttatggccac ttcctacgtg aaatcactgt ggcaaccggg ggtttcatat 1150

acactggaga agtcgtacat cgaatgctaa cagccacaca gtacatagca 1200

cctttaatgg caaatttcga tcccagtgta tccagaaatt caactgtcag 1250

atattttgat aatggcacag cacttgtggt ccagtgggac catgtacatc 1300

tccaggataa ttataacctg ggaagcttca cattccaggc aaccctgctc 1350

atggatggac gaatcatctt tggatacaaa gaaattcctg tcttggtcac 1400

acagataagt tcaaccaatc atccagtgaa agtcggactg tccgatgcat 1450

ttgtcgttgt ccacaggatc caacaaattc ccaatgttcg aagaagaaca 1500

atttatgaat accaccgagt agagctacaa atgtcaaaaa ttaccaacat 1550

ttcggctgtg gagatgaccc cattacccac atgcctccag tttaacagat 1600

gtggcccctg tgtatcttct cagattggct tcaactgcag ttggtgtagt 1650

aaacttcaaa gatgttccag tggatttgat cgtcatcggc aggactgggt 1700

ggacagtgga tgccctgaag agtcaaaaga gaagatgtgt gagaatacag 1750

aaccagtgga aacttcttct cgaaccacca caaccgtagg agcgacaacc 1800

acccagttca gggtcctaac taccaccaga agagcagtga cttctcagtt 1850

tcccaccagc ctccctacag aagatgatac caagatagca ctacatctaa 1900

aagataatgg agcttctaca gatgacagtg cagctgagaa gaaagggggga 1950

accctccacg ctggcctcat cattggaatc ctcatcctgg tcctcattgt 2000

agccacagcc attcttgtga cagtctatat gtatcaccac ccaacatcag 2050

cagccagcat cttctttatt gagagacgcc caagcagatg gcctgcgatg 2100

aagtttagaa gaggctctgg acatcctgcc tatgctgaag ttgaaccagt 2150

tggagagaaa gaaggcttta ttgtatcaga gcagtgctaa aatttctagg 2200

acagaacaac accagtactg gtttacaggt gttaagacta aaattttgcc 2250
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tatacctta agacaaacaa acaaacacac acacaaacaa gctctaagct 2300

gctgtagcct gaagaagaca agatttctgg acaagctcag cccaggaaac 2350

aaagggtaaa caaaaaacta aaacttatac aagataccat ttacactgaa 2400

catagaattc cctagtggaa tgtcatctat agttcactcg gaacatctcc 2450

cgtggactta tctgaagtat gacaagatta taatgctttt ggcttaggtg 2500

cagggttgca aagggatcag aaaaaaaaaa tcataataaa gctttagttc 2550

atgaggg 2557
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<210> 128
<211> 529
<212> PRT
<213> Homo Sapien

<400> 128

```
Met Ala Arg Phe Pro Lys Ala Asp Leu Ala Ala Ala Gly Val Met
  1               5                  10                  15

Leu Leu Cys His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly
                 20                  25                  30

Lys Pro Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln
                 35                  40                  45

Ala Phe Pro His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala
                 50                  55                  60

Tyr Ser His Arg Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val
                 65                  70                  75

Asp Thr Asn Arg Ala Ser Val Gly Gln Asp Ser Pro Glu Pro Arg
                 80                  85                  90

Ser Phe Thr Asp Leu Leu Leu Asp Asp Gly Gln Asp Asn Asn Thr
                 95                 100                 105

Gln Ile Glu Glu Asp Thr Asp His Asn Tyr Tyr Ile Ser Arg Ile
                110                 115                 120

Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp Leu Trp Val Asn Ile
                125                 130                 135

Asp Gln Met Glu Lys Asp Lys Val Lys Ile His Gly Ile Leu Ser
                140                 145                 150

Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser Phe Asp Phe
                155                 160                 165

Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala Thr Gly
                170                 175                 180

Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr Ala
                185                 190                 195
```

```
Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro Ser Val
             200             205             210

Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala Leu
             215             220             225

Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
             230             235             240

Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile
             245             250             255

Ile Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser
             260             265             270

Ser Thr Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val
             275             280             285

Val Val His Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr
             290             295             300

Ile Tyr Glu Tyr His Arg Val Glu Leu Gln Met Ser Lys Ile Thr
             305             310             315

Asn Ile Ser Ala Val Glu Met Thr Pro Leu Pro Thr Cys Leu Gln
             320             325             330

Phe Asn Arg Cys Gly Pro Cys Val Ser Ser Gln Ile Gly Phe Asn
             335             340             345

Cys Ser Trp Cys Ser Lys Leu Gln Arg Cys Ser Ser Gly Phe Asp
             350             355             360

Arg His Arg Gln Asp Trp Val Asp Ser Gly Cys Pro Glu Glu Ser
             365             370             375

Lys Glu Lys Met Cys Glu Asn Thr Glu Pro Val Glu Thr Ser Ser
             380             385             390

Arg Thr Thr Thr Thr Val Gly Ala Thr Thr Thr Gln Phe Arg Val
             395             400             405

Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln Phe Pro Thr Ser
             410             415             420

Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His Leu Lys Asp
             425             430             435

Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys Gly Gly
             440             445             450

Thr Leu His Ala Gly Leu Ile Ile Gly Ile Leu Ile Leu Val Leu
             455             460             465

Ile Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His
             470             475             480

Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser
```

103

```
                    485                  490                  495
Arg Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala
                500                  505                  510
Tyr Ala Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val
                515                  520                  525
Ser Glu Gln Cys
```

<210> 129
<211> 4834
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 3784
<223> unknown base

<400> 129

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ctcgaaccag tggctggcgg cggtgctcct cagcctgtgc tgcctgctac   100

cctcctgcct cccggctgga cagagtgtgg acttcccctg ggcggccgtg   150

gacaacatga tggtcagaaa aggggacacg gcggtgctta ggtgttattt   200

ggaagatgga gcttcaaagg gtgcctggct gaaccggtca agtattattt   250

ttgcgggagg tgataagtgg tcagtggatc ctcgagtttc aatttcaaca   300

ttgaataaaa gggactacag cctccagata cagaatgtag atgtgacaga   350

tgatggccca tacacgtgtt ctgttcagac tcaacataca cccagaacaa   400

tgcaggtgca tctaactgtg caagttcctc ctaagatata tgacatctca   450

aatgatatga ccgtcaatga aggaaccaac gtcactctta cttgtttggc   500

cactgggaaa ccagagcctt ccatttcttg gcgacacatc tccccatcag   550

caaaaccatt tgaaaatgga caatatttgg acatttatgg aattacaagg   600

gaccaggctg gggaatatga atgcagtgcg gaaaatgatg tgtcattccc   650

agatgtgagg aaagtaaaag ttgttgtcaa ctttgctcct actattcagg   700

aaattaaatc tggcaccgtg accccggac gcagtggcct gataagatgt   750

gaaggtgcag gtgtgccgcc tccagccttt gaatggtaca aaggagagaa   800

gaagctcttc aatggccaac aaggaattat tattcaaaat tttagcacaa   850

gatccattct cactgttacc aacgtgacac aggagcactt cggcaattat   900
```

104

```
acttgtgtgg ctgccaacaa gctaggcaca accaatgcga gcctgcctct 950

taaccctcca agtacagccc agtatggaat taccgggagc gctgatgttc 1000

ttttctcctg ctggtacctt gtgttgacac tgtcctcttt caccagcata 1050

ttctacctga agaatgccat tctacaataa attcaaagac ccataaaagg 1100

cttttaagga ttctctgaaa gtgctgatgg ctggatccaa tctggtacag 1150

tttgttaaaa gcagcgtggg atataatcag cagtgcttac atggggatga 1200

tcgccttctg tagaattgct cattatgtaa atactttaat tctactcttt 1250

tttgattagc tacattacct tgtgaagcag tacacattgt ccttttttta 1300

agacgtgaaa gctctgaaat tacttttaga ggatattaat tgtgatttca 1350

tgtttgtaat ctacaacttt tcaaaagcat tcagtcatgg tctgctaggt 1400

tgcaggctgt agtttacaaa aacgaatatt gcagtgaata tgtgattctt 1450

taaggctgca atacaagcat tcagttccct gtttcaataa gagtcaatcc 1500

acatttacaa agatgcattt ttttcttttt tgataaaaaa gcaaataata 1550

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ctcgcatgat attcaggttt caggaatgag ccttgtaata taactggctg 1650

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tcttacaatt tgaaagtaaa aataaaccag agtgatcaag ttaaaccata 1800

cactatctct aagtaacgaa ggagctattg gactgtaaaa atctcttcct 1850

gcactgacaa tggggtttga gaattttgcc ccacactaac tcagttcttg 1900

tgatgagaga caatttaata acagtatagt aaatatacca tatgatttct 1950

ttagttgtag ctaaatgtta gatccaccgt gggaaatcat tccctttaaa 2000

atgacagcac agtccactca aaggattgcc tagcaataca gcatcttttc 2050

ctttcactag tccaagccaa aaattttaag atgatttgtc agaaagggca 2100

caaagtccta tcacctaata ttacaagagt tggtaagcgc tcatcattaa 2150

ttttattttg tggcagctaa gttagtatga cagaggcagt gctcctgtgg 2200

acaggagcat tttgcatatt ttccatctga aagtatcact cagttgatag 2250

tctggaatgc atgttatata ttttaaaact tccaaaatat attataacaa 2300

acattctata tcggtatgta gcagaccaat ctctaaaata gctaattctt 2350
```

105

caataaaatc tttctatata gccatttcag tgcaaacaag taaaatcaaa 2400

aaagaccatc ctttattttt ccttacatga tatatgtaag atgcgatcaa 2450

ataaagacaa aacaccagtg atgagaatat cttaagataa gtaattatca 2500

aattattgtg aatgttaaat tatttctact ataaagaagc aaaactacat 2550

ttttgaagga aaatgctgtt actctaacat taatttacag gaatagtttg 2600

atggtttcac tctttactaa agaaaggcca tcaccttgaa agccatttta 2650

caggtttgat gaagttacca atttcagtac acctaaattt ctacaaatag 2700

tcccctttta caagttgtaa caacaaagac cctataataa aattagatac 2750

aagaaatttt gcagtggtta tacatatttg agatatctag tatgttgccc 2800

tagcagggat ggcttaaaaa ctgtgatttt ttttcttcaa gtaaaactta 2850

gtcccaaagt acatcataaa tcaattttaa ttagaaaaat gaatcttaaa 2900

tgaggggaca taagtatact ctttccacaa aatggcaata ataaggcata 2950

aagctagtaa atctactaac tgtaataaat gtatgacatt attttgattg 3000

atacattaaa aaagagtttt tagaacaaat atggcattta actttattat 3050

ttatttgctt ttaagaaata ttctttgtgg aattgttgaa taaactataa 3100

aatattattt tgtattgcag ctttaaagtg gcacactcca taataatcta 3150

cttactagaa atagtggtgc taccacaaaa aatgttaacc atcagtacca 3200

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ggtataaact atggatgaac caaataatta gttcaaagtg ttgtcatgat 3350

tccaaatttg tggagtctgg tgtttttacc atagaatgtg acagaagtac 3400

agtcatagct cagtagctat atgtatttgc ctttatgtta gaagagactt 3450

tcttgagtga catttttaaa tagaggaggt attcactatg tttttctgta 3500

tcacagcagc attcctagtc cttaggccct cggacagagt gaaatcatga 3550

gtatttatga gttcaatatt gtcaaataag gctacagtat ttgctttttt 3600

gtgtgaatgt attgcatata atgttcaagt agatgatttt acatttatgg 3650

acatataaaa tgtctgatta ccccatttta tcagtcctga ctgtacaaga 3700

ttgttgcaat ttcagaatag cagttttata aattgattta tcttttaatc 3750

tataacaatt tgtgttagct gttcatttca ggantatatt ttctacaagt 3800

106

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tccacttgtg ggactccttt tgttgcccct attttttttt aaagaaggaa 3850

gaaagaaaaa taagtagcag tttaaaaatg agaatggaga gaaaagaaaa 3900

agaatgaaaa ggaaaggcag taaagaggga aaaaaaagga aggatggaag 3950

gaatgaagga aggaagggag gaaggggaga aggtaggaag aaagaaagga 4000

tgagagggaa ggaagaatca gagtattagg gtagttaact tacacatttg 4050

cattcttagt ttaactgcaa gtggtgtaac tatgtttttc aatgatcgca 4100

tttgaaacat aagtcctatt ataccattaa gttcctatta tgcagcaatt 4150

atataataaa aagtactgcc caagttatag taatgtgggt gtttttgaga 4200

cactaaaaga tttgagaggg agaatttcaa acttaaagcc acttttgggg 4250

ggtttataac ttaactgaaa aattaatgct tcatcataac atttaagcta 4300

tatctagaaa gtagactgga gaactgagaa aattacccag gtaattcagg 4350

gaaaaaaaaa aatatatata tatataaata cccctacatt tgaagtcaga 4400

aaactctgaa aaactgaatt atcaaagtca atcatctata atgatcaaat 4450

ttactgaaca attgttaatt tatccattgt gcttagcttt gtgacacagc 4500

caaaagttac ctatttaatc ttttcaataa aaattgtttt ttgaaatcca 4550

gaaatgattt aaaaagaggt caggttttta actatttatt gaagtatgtg 4600

gatgtacagt atttcaatag atatgaatat gaataaatgg tatgccttaa 4650

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cttttagtaa aacatccata tttcataacc tgatgtaaaa tatgttgtac 4750

tgtttccaat aggtgaatat aaactcagtt tatcaattaa aaaaaaaaaa 4800

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 4834
```

<210> 130
<211> 354
<212> PRT
<213> Homo Sapien

<400> 130

```
Met Asp Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln
1               5                  10                  15

Trp Leu Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser
            20                  25                  30

Cys Leu Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val
            35                  40                  45

Asp Asn Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys
```

```
                50                        55                        60
Tyr Leu Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser
                65                        70                        75

Ser Ile Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg
                80                        85                        90

Val Ser Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile
                95                       100                       105

Gln Asn Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val
               110                       115                       120

Gln Thr Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val
               125                       130                       135

Gln Val Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val
               140                       145                       150

Asn Glu Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys
               155                       160                       165

Pro Glu Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys
               170                       175                       180

Pro Phe Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg
               185                       190                       195

Asp Gln Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Asp Val Ser
               200                       205                       210

Phe Pro Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro
               215                       220                       225

Thr Ile Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser
               230                       235                       240

Gly Leu Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe
               245                       250                       255

Glu Trp Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly
               260                       265                       270

Ile Ile Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr
               275                       280                       285

Asn Val Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala
               290                       295                       300

Asn Lys Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro
               305                       310                       315

Ser Thr Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe
               320                       325                       330

Ser Cys Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile
               335                       340                       345
```

108

Phe Tyr Leu Lys Asn Ala Ile Leu Gln
                    350

<210> 131
<211> 823
<212> DNA
<213> Homo Sapien

<400> 131
 atagtagaag aatgtctctg aaattactgg atgagtttca gtcatacttt 50

 cacatgggca caatttcaca ttcaagctcc ttatcctagg ctaattttat 100

 attatgttaa atcacttgtt tttgttctca cggcttcctg cctgctatag 150

 gcataattac gaggaagcag aacttctcca gaagcaagcg cacatgcgtt 200

 ccaaaataag agcaaattcg ctctaaacac aggaaaagac ctgaagcttt 250

 aattaagggg ttacatccaa ccccagagcg cttttgtggg cactgattgc 300

 tccagcttct gcgtcactgc gcgagggaag agggaagagg atccaggcgt 350

 tagacatgta tagacacaaa aacagctgga gattgggctt aaaataccca 400

 ccaagctcca aagaagagac ccaagtcccc aaaacattga tttcagggct 450

 gccaggaagg aagagcagca gcagggtggg agagaagctc cagtcagccc 500

 acaagatgcc attgtccccc ggcctcctgc tgctgctgct ctccggggcc 550

 acggccaccg ctgccctgcc cctggagggt ggccccaccg ccgagacag 600

 cgagcatatg caggaagcgg caggaataag gaaaagcagc ctcctgactt 650

 tcctcgcttg gtggtttgag tggacctccc aggccagtgc cgggcccctc 700

 ataggagagg aagctcggga ggtggccagg cggcaggaag gcgcacccc 750

 ccagcaatcc gcgcgccggg acagaatgcc ctgcaggaac ttcttctgga 800

 agaccttctc ctcctgcaaa tag 823

<210> 132
<211> 155
<212> PRT
<213> Homo Sapien

<400> 132
 Met Tyr Arg His Lys Asn Ser Trp Arg Leu Gly Leu Lys Tyr Pro
   1   5   10   15

 Pro Ser Ser Lys Glu Glu Thr Gln Val Pro Lys Thr Leu Ile Ser
                 20   25   30

 Gly Leu Pro Gly Arg Lys Ser Ser Ser Arg Val Gly Glu Lys Leu
                 35   40   45

```
Gln Ser Ala His Lys Met Pro Leu Ser Pro Gly Leu Leu Leu Leu
                50              55                      60

Leu Leu Ser Gly Ala Thr Ala Thr Ala Ala Leu Pro Leu Glu Gly
                65              70                      75

Gly Pro Thr Gly Arg Asp Ser Glu His Met Gln Glu Ala Ala Gly
                80              85                      90

Ile Arg Lys Ser Ser Leu Leu Thr Phe Leu Ala Trp Trp Phe Glu
                95              100                     105

Trp Thr Ser Gln Ala Ser Ala Gly Pro Leu Ile Gly Glu Glu Ala
                110             115                     120

Arg Glu Val Ala Arg Arg Gln Glu Gly Ala Pro Pro Gln Gln Ser
                125             130                     135

Ala Arg Arg Asp Arg Met Pro Cys Arg Asn Phe Phe Trp Lys Thr
                140             145                     150

Phe Ser Ser Cys Lys
                155
```

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
 tcagggctgc caggaaggaa gagc 24

<210> 134
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 134
 gcaggaggag aaggtcttcc agaagaag 28

<210> 135
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 135
 agaagttcca gtcagcccac aagatgccat tgtcccccgg cctcc 45

<210> 136

<211> 1875
<212> DNA
<213> Homo Sapien

<400> 136
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gtcgtgtgct tggaggaagc cgcggaaccc ccagcgtccg tccatggcgt 50

ggagccttgg gagctggctg ggtggctgcc tgctggtgtc agcattggga 100

atggtaccac ctccccgaaaa tgtcagaatg aattctgtta atttcaagaa 150

cattctacag tgggagtcac ctgcttttgc caaagggaac ctgactttca 200

cagctcagta cctaagttat aggatattcc aagataaatg catgaatact 250

accttgacgg aatgtgattt ctcaagtctt tccaagtatg gtgaccacac 300

cttgagagtc agggctgaat ttgcagatga gcattcagac tgggtaaaca 350

tcaccttctg tcctgtggat gacaccatta ttggacccccc tggaatgcaa 400

gtagaagtac ttgctgattc tttacatatg cgtttcttag cccctaaaat 450

tgagaatgaa tacgaaactt ggactatgaa gaatgtgtat aactcatgga 500

cttataatgt gcaatactgg aaaaacggta ctgatgaaaa gtttcaaatt 550

actccccagt atgactttga ggtcctcaga aacctggagc catggacaac 600

ttattgtgtt caagttcgag ggtttcttcc tgatcggaac aaagctgggg 650

aatggagtga gcctgtctgt gagcaaacaa cccatgacga aacggtcccc 700

tcctggatgg tggccgtcat cctcatggcc tcggtcttca tggtctgcct 750

ggcactcctc ggctgcttct ccttgctgtg gtgcgtttac aagaagacaa 800

agtacgcctt ctcccctagg aattctcttc cacagcacct gaaagagttt 850

ttgggccatc ctcatcataa cacacttctg tttttctcct ttccattgtc 900

ggatgagaat gatgtttttg acaagctaag tgtcattgca gaagactctg 950

agagcggcaa gcagaatcct ggtgacagct gcagcctcgg accccgcct 1000

gggcaggggc cccaaagcta ggctctgaga aggaaacaca ctcggctggg 1050

cacagtgacg tactccatct cacatctgcc tcagtgaggg atcagggcag 1100

caaacaaggg ccaagaccat ctgagccagc cccacatcta gaactccaga 1150

cctggactta gccaccagag agctacattt taaaggctgt cttggcaaaa 1200

atactccatt tgggaactca ctgccttata aaggctttca tgatgttttc 1250

agaagttggc cactgagagt gtaattttca gccttttata tcactaaaat 1300

aagatcatgt tttaattgtg agaaacaggg ccgagcacag tggctcacgc 1350
```

111

ctgtaatacc agcaccttag aggtcgaggc aggcggatca cttgaggtca 1400

ggagttcaag accagcctgg ccaatatggt gaaacccagt ctctactaaa 1450

aatacaaaaa ttagctaggc atgatggcgc atgcctataa tcccagctac 1500

tcgagtgcct gaggcaggag aattgcatga acccgggagg aggaggagga 1550

ggttgcagtg agccgagata gcggcactgc actccagcct gggtgacaaa 1600

gtgagactcc atctcaaaaa aaaaaaaaaa aaattgtgag aaacagaaat 1650

acttaaaatg aggaataaga atggagatgt tacatctggt agatgtaaca 1700

ttctaccaga ttatggatgg actgatctga aaatcgacct caactcaagg 1750

gtggtcagct caatgctaca cagagcacgg acttttggat tctttgcagt 1800

actttgaatt tattttcta cctatatatg ttttatatgc tgctggtgct 1850

ccattaaagt tttactctgt gttgc 1875

<210> 137
<211> 325
<212> PRT
<213> Homo Sapien

<400> 137

```
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val
 1               5              10                  15

Ser Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn
            20              25                  30

Ser Val Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe
            35              40                  45

Ala Lys Gly Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg
            50              55                  60

Ile Phe Gln Asp Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp
            65              70                  75

Phe Ser Ser Leu Ser Lys Tyr Gly Asp His Thr Leu Arg Val Arg
            80              85                  90

Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val Asn Ile Thr Phe
            95              100                 105

Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly Met Gln Val
            110             115                 120

Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala Pro Lys
            125             130                 135

Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr Asn
            140             145                 150
```

```
Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu
            155             160                         165

Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn
            170             175                         180

Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
            185             190                         195

Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu
            200             205                         210

Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val
            215             220                         225

Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly
            230             235                         240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala
            245             250                         255

Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu
            260             265                         270

Gly His Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu
            275             280                         285

Ser Asp Glu Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu
            290             295                         300

Asp Ser Glu Ser Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu
            305             310                         315

Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser
            320             325
```

<210> 138
<211> 2570
<212> DNA
<213> Homo Sapien

<400> 138

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cgagcgccaa cccgctagcg cctgaatccg gcgtgctgcc cgctcgccgc  50

ccgccatggc ccgcgcagcc ccgctgctcg ccgcgttgac cgcgctcctc  100

gccgccgccg ctgctggcgg agatgccccg ccgggcaaaa tcgcggtggt  150

tggggctggg attgggggct ctgctgtggc ccattttctc cagcagcact  200

ttggacctcg ggtgcagatc gacgtgtacg agaagggaac cgtgggtggc  250

cgcttggcca ccatctcagt caacaagcag cactatgaga gcggggctgc  300

ctccttccac tccctgagcc tgcacatgca ggacttcgtc aagctgctgg  350

ggctgaggca ccggcgcgag gtggtgggca ggagcgccat cttcggcggg  400
```

```
gagcacttca tgctggagga gactgactgg tacctgctga acctcttccg 450

cctctggtgg cactatggca tcagcttcct gaggctgcag atgtgggtgg 500

aggaggtcat ggagaagttc atgaggatct ataagtacca ggcccacggc 550

tatgccttct cgggtgtgga ggagctgctc tactcactgg gggagtccac 600

ctttgttaac atgacccagc actctgtggc tgagtccctg ctgcaggtgg 650

gcgtcacgca gcgctttatt gatgatgtcg tttctgctgt cctgcgggcc 700

agctatggcc agtcagcagc gatgcccgcc tttgcaggag ccatgtcact 750

agccggggcc caaggcagcc tgtggtctgt ggaaggaggc aataagctgg 800

tttgttccgg tttgctgaag ctcaccaagg ccaatgtgat ccatgccaca 850

gtgacctctg tgaccctgca cagcacagag gggaaagccc tgtaccaggt 900

ggcgtatgag aatgaggtag gcaacagctc tgacttctat gacatcgtgg 950

tcatcgccac cccccctgcac ctggacaaca gcagcagcaa cttaaccttt 1000

gcaggcttcc acccgcccat tgatgacgtg cagggctctt ccagcccac 1050

cgtcgtctcc ttggtccacg gctacctcaa ctcgtcctac ttcggtttcc 1100

cagaccctaa gcttttcccc tttgccaaca tccttaccac agatttcccc 1150

agcttcttct gcactctgga caacatctgc cctgtcaaca tctctgccag 1200

cttccggcga aagcagcccc aggaggcagc tgtttggcga gtccagtccc 1250

ccaagcccct ctttcggacc cagctaaaga ccctgttccg ttcctattac 1300

tcagtgcaga cagctgagtg gcaggcccat cccctctatg gctcccgccc 1350

cacgctcccg aggtttgcac tccatgacca gctcttctac ctcaatgccc 1400

tggagtgggc ggccagctcc gtggaggtga tggccgtggc tgccaagaat 1450

gtggccttgc tggcttacaa ccgctggtac caggacctag acaagattga 1500

tcaaaaagat ttgatgcaca aggtcaagac tgaactgtga gggctctagg 1550

gagagcctgg gaactttcat cccccactga agatggatca tcccacagca 1600

gcccaggact gaataagcca tgctcgccca ccaggcttct ttctgacccc 1650

tcatgtatca agcatctcca ggtgacctac tgtctgccta tattaagggt 1700

ccacacggcg gctgctgctt tttttaagg gggaaagtaa gaaaagagaa 1750

ggaaatccaa gccagtatat ttgtttatt tattttttt aagaagaaaa 1800

aagttcatct tcacaaggtg cttcagactt ggtttcttag ctagaaacca 1850
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114

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gaagactacg ggagggaata taaggcagag aactatgagt cttattttat 1900

tactgttttt cactacctac tcccacaatg gacaatcaat tgaggcaacc 1950

tacaagaaaa catttacaac cagatggtta caaataaagt agaagggaag 2000

atcagaaaac ctaagaaatg atcatagctc ctggttactg tggacttgat 2050

ggatttgaag tacctagttc agaactccct agtcaccatc tccaagcctg 2100

tcaacatcac tgcatattgg aggagatgac tgtggtagga cccaaggaag 2150

agatgtgtgc ctgaatagtc gtcaccatat ctccaagctt cctggcaacc 2200

agtgggaaaa gaaacatgcg aggctgtagg aagagggaag ctcttccttg 2250

gcacctagag gaattagcca ttctcttcct tatgcaaaga ttgaggaatg 2300

caacaatata aagaagagaa gtccccagat ggtagagagc agtcatatct 2350

tacccctaga tgttcatccc agcagaagaa agaagaaggt gttggggtag 2400

gattcttcag aggttagcct ggtactttct catcagacac tagcttgaag 2450

taagaggaga attatgcttt tctttgcttt ttctacaaac ccttaaaaat 2500

cacttgtttt aaaaagaaag taaaagccct tttcattcaa aaaaaaaaaa 2550

aaaaaaaaaa aaaaaaaaaa 2570
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<210> 139
<211> 494
<212> PRT
<213> Homo Sapien

<400> 139

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Ala Ala Ala Ala Ala Gly Gly Asp Ala Pro Pro Gly Lys Ile Ala
            20                  25                  30

Val Val Gly Ala Gly Ile Gly Gly Ser Ala Val Ala His Phe Leu
            35                  40                  45

Gln Gln His Phe Gly Pro Arg Val Gln Ile Asp Val Tyr Glu Lys
            50                  55                  60

Gly Thr Val Gly Gly Arg Leu Ala Thr Ile Ser Val Asn Lys Gln
            65                  70                  75

His Tyr Glu Ser Gly Ala Ala Ser Phe His Ser Leu Ser Leu His
            80                  85                  90

Met Gln Asp Phe Val Lys Leu Leu Gly Leu Arg His Arg Arg Glu
            95                  100                 105

Val Val Gly Arg Ser Ala Ile Phe Gly Gly Glu His Phe Met Leu
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115

```
                      110                 115                 120
Glu Glu Thr Asp Trp Tyr Leu Leu Asn Leu Phe Arg Leu Trp Trp
                  125                 130                 135
His Tyr Gly Ile Ser Phe Leu Arg Leu Gln Met Trp Val Glu Glu
                  140                 145                 150
Val Met Glu Lys Phe Met Arg Ile Tyr Lys Tyr Gln Ala His Gly
                  155                 160                 165
Tyr Ala Phe Ser Gly Val Glu Glu Leu Leu Tyr Ser Leu Gly Glu
                  170                 175                 180
Ser Thr Phe Val Asn Met Thr Gln His Ser Val Ala Glu Ser Leu
                  185                 190                 195
Leu Gln Val Gly Val Thr Gln Arg Phe Ile Asp Asp Val Val Ser
                  200                 205                 210
Ala Val Leu Arg Ala Ser Tyr Gly Gln Ser Ala Ala Met Pro Ala
                  215                 220                 225
Phe Ala Gly Ala Met Ser Leu Ala Gly Ala Gln Gly Ser Leu Trp
                  230                 235                 240
Ser Val Glu Gly Gly Asn Lys Leu Val Cys Ser Gly Leu Leu Lys
                  245                 250                 255
Leu Thr Lys Ala Asn Val Ile His Ala Thr Val Thr Ser Val Thr
                  260                 265                 270
Leu His Ser Thr Glu Gly Lys Ala Leu Tyr Gln Val Ala Tyr Glu
                  275                 280                 285
Asn Glu Val Gly Asn Ser Ser Asp Phe Tyr Asp Ile Val Val Ile
                  290                 295                 300
Ala Thr Pro Leu His Leu Asp Asn Ser Ser Ser Asn Leu Thr Phe
                  305                 310                 315
Ala Gly Phe His Pro Pro Ile Asp Asp Val Gln Gly Ser Phe Gln
                  320                 325                 330
Pro Thr Val Val Ser Leu Val His Gly Tyr Leu Asn Ser Ser Tyr
                  335                 340                 345
Phe Gly Phe Pro Asp Pro Lys Leu Phe Pro Phe Ala Asn Ile Leu
                  350                 355                 360
Thr Thr Asp Phe Pro Ser Phe Phe Cys Thr Leu Asp Asn Ile Cys
                  365                 370                 375
Pro Val Asn Ile Ser Ala Ser Phe Arg Arg Lys Gln Pro Gln Glu
                  380                 385                 390
Ala Ala Val Trp Arg Val Gln Ser Pro Lys Pro Leu Phe Arg Thr
                  395                 400                 405
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116

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Gln Leu Lys Thr Leu Phe Arg Ser Tyr Tyr Ser Val Gln Thr Ala
                410                 415                 420

Glu Trp Gln Ala His Pro Leu Tyr Gly Ser Arg Pro Thr Leu Pro
                425                 430                 435

Arg Phe Ala Leu His Asp Gln Leu Phe Tyr Leu Asn Ala Leu Glu
                440                 445                 450

Trp Ala Ala Ser Ser Val Glu Val Met Ala Val Ala Ala Lys Asn
                455                 460                 465

Val Ala Leu Leu Ala Tyr Asn Arg Trp Tyr Gln Asp Leu Asp Lys
                470                 475                 480

Ile Asp Gln Lys Asp Leu Met His Lys Val Lys Thr Glu Leu
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 141
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
 caggcttaca atgttatgat cagaca   26

<210> 142
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<220>
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<400> 142
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<220>
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<400> 143
 ggccttgcag acaaccgt 18

<210> 144
<211> 21
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 144
 cagactgagg gagatccgag a 21

<210> 145
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<213> Artificial Sequence

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<400> 145
 gcagattttg aggacagcca cctcca 26

<210> 146
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<400> 146
 catcaagcgc ctctacca 18

<210> 147
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<400> 147
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<210> 148
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<400> 148
 cagctgccct tccccaacca 20

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<220>
<223> Synthetic oligonucleotide probe

<400> 149
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<210> 150
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 150
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<210> 151
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 151
 caggccccct tgatctgtac ccca 24
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119